



```

1 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCCTG
51 CGCCAGGATG GAGTTCGTGA AATGCCCTGG CCACCCGAA GAGTTCCTACA
101 ACCTGGTGCG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
151 GACCAGGACT CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA
201 TCAGACCACT CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGGAAA
251 TGCACAACGC AGTGTGCATA TTTTATCTGG TTCTCCGAGC TCTGGACACA
301 CTGGAAGATG ACATGACCAT CAGTGTGGAA AAGAAGGTCC CGCTGTACAA
351 CAACTTTCAC TCTTTCCTTT ACCAACCAGA CTGGCGGTTT ATGGAGAGCA
401 AGGAGAAGGA TCGCCAGGTG CTGGAGGACT TCCCAACGTA CTGCCACTAT
451 GTTGCTGGGC ATGGCCGAAAT TGGCCTTTCC CGTCTTTTCT CAGCCTCAGA
501 GTTTGAAGAC CCCTTAGTTG GTGAAGATAC AGAACGTGCC AACTCTATGG
551 GCCTGTTTCT GCAGAAAACA AACATCATCC GTGACTATCT GGAAGACCAG
601 CAAGGAGGAA GAGAGTTCTG GCCTCAAGAG GTTTGGAGCA GGTATGTTAA
651 GAAGTTAGGG GATTTTGCCTA AGCCGGAGAA TATTGACTTG GCCGTGCAGT
701 GCCTGAATGA ACTTATAACC AATGCACTGC ACCACATCCC AGATGTCATC
751 ACCTACCTTT CGAGACTCAG AAACCAGAGT GTGTTTAACT TCTGTGCTAT
801 TCCACAGGTG ATGGCCATG CCACTTTGGC TGCCCTGTTAT AATAACCAGC
851 AGGTGTTCAA AGGGGCAGTG AAGATTCGGA AAGGGCAAGC AGTGACCCCTC
901 ATGATGGATG CCACCAATAT GCCAGCTGTC AAAGCCATCA TATATCAGTA
951 TATGGAAGAG ATTTATCATA GAATCCCCGA CTCAGACCCA TCTTCTAGCA
1001 AAACAAGGCA GATCATCTCC ACCATCCGGA CGCAGAATCT TCCCAACTGT
1051 CAGCTGATTT CCCGAAGCCA CTACTCCCCC ATCTACCTGT CGTTTGTCTAT
1101 GCTTTTGGCT GCCCTGAGCT GGCAGTACCT GACCACTCTC TCCCAGGTAA
1151 CAGAAGACTA TGTTTCAGACT GGAGAACACT GATCCCAAAT TTGTCCATAG
1201 CTGAAGTCCA CCATAAAGTG GATTTACTTT TTTTCTTTAA GGATGGATGT
1251 TGTGTTCTCT TTATTTTCTT CCTACTACTT TAATCCCTAA AAGAACGCTG
1301 TGTGGCTGGG ACCTTTAGGA AAGTGAAATG CAGGTGAGAA GAACCTAAAC
1351 ATGAAAGGAA AGGGTGCCCTC ATCCCAGCAA CCTGTCCCTG TGGGTGATGA
1401 TCACTGTGCT GCTTGGCGCT CATGGCAGAG CATTGAGTGC CACGGTTTAG
1451 GTGAAGTCGC TGCATATGTT ACTGTCATGA GATCCTACTT AGTATGATCC
1501 TGGCTAGAAAT GATAATTAAA AGTATTTAAT TTGAAAAAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1601 AAAAAA (SEQ ID NO:1)

```

#### FEATURES:

5'UTR: 1-57  
Start Codon: 58  
Stop Codon: 1180  
3'UTR: 1183

#### Homologous proteins:

##### Top 10 BLAST Hits

	Score	E
CRA 108000024649260 /altid=gi 12734163 /def=ref XP_005134.2  fa...	770	0.0
CRA 18000004925908 /altid=gi 4758350 /def=ref NP_004453.1  farn...	743	0.0
CRA 18000004929946 /altid=gi 2135096 /def=pir  I38245 farnesyl-...	741	0.0
CRA 18000004993865 /altid=gi 2136196 /def=pir  I52090 squalene ...	740	0.0
CRA 18000004932414 /altid=gi 6753838 /def=ref NP_034321.1  farn...	671	0.0
CRA 18000004937535 /altid=gi 9506591 /def=ref NP_062111.1  farn...	654	0.0
CRA 1000682330885 /altid=gi 6002565 /def=gb AAF00038.1  (AF0903...	582	e-165
CRA 335001098694081 /altid=gi 11514495 /def=pdb 1EZFA Chain A,...	579	e-164
CRA 18000005103884 /altid=gi 2463565 /def=dbj BAA22557.1  (AB00...	282	1e-74
CRA 18000005103885 /altid=gi 7434086 /def=pir  T00489 farnesyl-...	280	4e-74

FIGURE 1A

BLAST dbEST hits:

	Score	E
gi 12926380 /dataset=dbest /taxon=960...	1441	0.0
gi 12945082 /dataset=dbest /taxon=960...	1370	0.0
gi 12921315 /dataset=dbest /taxon=960...	1346	0.0
gi 11642571 /dataset=dbest /taxon=96...	1330	0.0
gi 9141948 /dataset=dbest /taxon=9606...	1281	0.0
gi 13040072 /dataset=dbest /taxon=960...	1233	0.0
gi 12944143 /dataset=dbest /taxon=960...	1055	0.0

**EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

From BLAST dbEST hits:

gi|12926380 placenta  
gi|12945082 T cells from T cell leukemia  
gi|12921315 Fetal brain  
gi|11642571pancreas  
gi|9141948 Burkitt lymphoma  
gi|13040072 bladder

From tissue screening panels:

Whole liver

FIGURE 1B

1 MEFVKCLGHP EEFYNLVRFR IGGKRKVMPPK MDQDSLSSSL KTCYKYLNQ  
51 SRSFAAVIQA LDGEMRNAV C IFYLVLRALD TLEDDMTISV EKKVPLLHNF  
101 HSFLYQPDWR FMESKEKDRQ VLEDFPTYCH YVAGLVGIGL SRLFSASEFE  
151 DPLVGEDTER ANSMGLFLQK TNIIRDYLED QGGREFWPQ EVWSRYVKKL  
201 GDFAKPENID LAVQCLNELI TNALHHIPDV ITYLSRLRNQ SVFNFCAIPQ  
251 VMAIATLAAC YNNQVFKGA VKIRKGQAVT LMMDATNMPA VKAIIYQYME  
301 EIYHRIPDS PSSSKTRQII STIRTQNLPN CQLISRSHYS PIYLSFVMLL  
351 AALSWQYLTT LSQVTEDYVQ TGEH (SEQ ID NO:2)

**FEATURES:**

**Functional domains and key regions:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

Number of matches: 2

1 48-51 NQTS  
2 239-242 NQSV

[2] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 5

1 39-41 SLK  
2 50-52 TSR  
3 158-160 TER  
4 313-315 SSK  
5 322-324 TIR

[3] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 3

1 81-84 TLED  
2 145-148 SASE  
3 147-150 SEFE

[4] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 2

1 137-142 GIGLSR  
2 276-281 GQAVTL

[5] PDOC00009 PS00009 AMIDATION  
Amidation site

22-25 GGKR

[6] PDOC00802 PS01044 SQUALEN\_PHYTOEN\_SYN\_1  
Squalene and phytoene synthases signature 1

128-143 YCHYVAGLVGIGLSRL

[7] PDOC00802 PS01045 SQUALEN\_PHYTOEN\_SYN\_2  
Squalene and phytoene synthases signature 2

164-189 MGLFLQKTNIIRDYLEDQGGREFWP

**Membrane spanning structure and domains:**

Helix	Begin	End	Score	Certainty
1	125	145	0.834	Putative
2	241	261	1.467	Certain
3	339	359	1.716	Certain

FIGURE 2B

**BLAST Alignment to Top Hit:**

```
>CRA|18000004925908 /altid=gi|4758350 /def=ref|NP_004453.1|
      farnesyl-diphosphate farnesyltransferase 1;
      Farnesyl-diphosphate farnesyltransferase 1 (squalene
      synthase); Squalene synthase [Homo sapiens] /org=Homo
      sapiens /taxon=9606 /dataset=nraa /length=417
      Length = 417

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1  MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60
      MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA
Sbjct: 1  MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60

Query: 61  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
      LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 61  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT-----YCHYVAGLVG 137
      VLEDFPT YCHYVAGLVG
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197
      IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 240

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFC AIPQVMAIATL 257
      KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFC AIPQVMAIATL
Sbjct: 241 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFC AIPQVMAIATL 300

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317
      AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR
Sbjct: 301 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 360

Query: 318 QIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEYVQTGEH 374
      QIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEYVQTGEH
Sbjct: 361 QIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEYVQTGEH 417 (SEQ ID
NO:4)
```

```
>CRA|108000024649260 /altid=gi|12734163 /def=ref|XP_005134.2|
      farnesyl-diphosphate farnesyltransferase 1 [Homo
      sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
      /length=431
      Length = 431

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1  MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60
      MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA
Sbjct: 15  MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 74

Query: 61  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
      LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 75  LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 134

Query: 121 VLEDFPT-----YCHYVAGLVG 137
      VLEDFPT YCHYVAGLVG
Sbjct: 135 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 194
```

FIGURE 2C

Query: 138 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 197  
IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV  
Sbjct: 195 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 254

Query: 198 KKLGDFAK PENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257  
KKLGDFAK PENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL  
Sbjct: 255 KKLGDFAK PENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 314

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317  
AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR  
Sbjct: 315 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 374

Query: 318 QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLTTL SQVTEDYVQTGEH 374  
QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLTTL SQVTEDYVQTGEH  
Sbjct: 375 QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLTTL SQVTEDYVQTGEH 431 (SEQ ID NO:5)

>CRA|18000004929946 /altid=gi|2135096 /def=pir||I38245  
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21),  
hepatic - human /org=human /taxon=9606 /dataset=nraa  
/length=417  
Length = 417

Score = 741 bits (1893), Expect = 0.0  
Identities = 373/417 (89%), Positives = 373/417 (89%), Gaps = 43/417 (10%)

Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYL NQTSRSFAAVIQA 60  
MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYL NQTSRSFAAVIQA  
Sbjct: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYL NQTSRSFAAVIQA 60

Query: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120  
LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ  
Sbjct: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT-----YCHYVAGLVG 137  
VLEDFPT YCHYVAGLVG  
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 197  
IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV  
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQQGGREFWPQEVWSRYV 240

Query: 198 KKLGDFAK PENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 257  
KKLGDFAK PENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL  
Sbjct: 241 KKLGDFAK PENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATL 300

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317  
AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR  
Sbjct: 301 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 360

Query: 318 QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLTTL SQVTEDYVQTGEH 374  
QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLTTL SQVTEDYVQTGEH  
Sbjct: 361 QIISTIRTQNL PNCQLISRSHYSPIYLSFVMLLAALSWQYLTTL SQVTEDYVQTGEH 417 (SEQ ID NO:6)

FIGURE 2D

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00494	Squalene and phytoene synthases	425.8	4e-124	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00494	1/2	47	126 ..	1	88 [.	124.6	1.1e-33
PF00494	2/2	127	291 ..	146	317 .]	301.1	1.3e-86

FIGURE 2E

```
1 TATTTATTCC TAATTAAATG GGGAGGAAAG TCTTTGAAGA GGAACCTCTA
51 CTTTACTTTT TATACCGTCA TGGCTGGAAA CTAAGTTTTT AAGATTTTTT
101 TGGGGTTCCC TTGGCCGAGG TGGGGAGTGG GAGGGCTGTC CAGTGGTAGG
151 GACTTAGGAT TTTTAGTTTA CAGTAGTAGG GGAAACACTC TGTAATCTAA
201 TACATAAGTA AATGATGTAT TAGAATATGG TAAATATAGG CAAGTAGACC
251 CCCACTGGGA TTAGCAGTGG TGGAAATGTG AGAGAGGGCA AACAGGTGGG
301 TCTAGATGAG GTGTGAGCAG ACTCGAGGGG CACAGGAGTT AGTCAAGCCA
351 GTATCTGGGG GATAGTGCAG GAATAGTGAA CAGCTAGACA AAAAGTCCTA
401 GGGCCAGAGA AAGCAAAAGC ATAAGAGATG GAGGCCAGAG AGGTAATCTG
451 GGTGGAAGGC TGCAGCCTCT CAGGATCCCT ATAGGTGCTT TGGCTTTTGT
501 TGGAGAGACA CTGAACAGCT TTGGGCAGTG AACGTACCTG ACAGGTTTCC
551 TGTTTGTTTT TGAGATGAAG TCTCGCTCTT GTCCCCCAGG CTGGAGTGCA
601 ATAGCGCGAT CTCAGCTCAC TGCAACCTCT GCCTCCTGTG TTCAAGCGAT
651 TCTCCTGCCT CAGCCTCCCA GGTAGCTGGG ATTATAGGCG CCTGCCACCA
701 TGCCTGGCTA ATTTTGTAT TTTTAGTAGA GACGCAGTTT CAGCATGTTG
751 GCCAGGCTGG TCTTGAACCT CAGACCTCAG GTGATCCGCC CGCCTTGGCC
801 TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCGCTC GGCTAGACCT
851 GACAGGTTTT AAAAGGATTA CTGGTTGCTG TGTTAAAACA GACTGCAGGA
901 TGGCTTAGGT AGCCAGTAGG TTTTTTTTTT TTTTGGAGAC GTAGTCTTGC
951 TCTGTTGGCC TGGCTGGAGT GCAGCGGTGT CATCTTGGCT CACTGCAAAC
1001 TCCGCTTCCC GGGTTCAAGT GATTCTCCTG CCTCAGCCTC CGGAGTAGTT
1051 GGGACTACAG GCGCCACCA CCACACTCGG CTTTTTTGTA TTTTGTAGT
1101 AGACGGGTTT CACCATGTTG GCCAGGATGG TCTCGATCTC TTGACCTCGT
1151 GATCCACCCG CCTTGGCCTC CCAAAGTGTT GCGATTACAG GCGTGAGCCA
1201 CCACGCCTGG ACGGGTAGCC AGTAGTTTCT AGGGCTGGAG AGATCTAGGA
1251 TGAGAGAAGT TTCCACATTC CTGTTACAGG CTCTCTAAGG CTTCAGCTCC
1301 TTTTCTTAGG ACTAAGCTGG ATCTCAAGTA AACACTAGAG AGGGGGCAGC
1351 TGAAGCTCCA GGAGTGTGTG GGGCTCCCTG GGGCTGGATG GCGGTGGCGG
1401 GCAGCGCAGC TGGGCTGTGC TCGGGTGTGT TACAGTAAAG ACGCCAGCT
1451 TGGCGCTGGC CCGGCCTTTT CACGGTTTTA GGCTCTACAG AGAGCGGCTG
1501 CAGAGCTCAC CCGGCTGGCA GGAGCCACCG AGGCCGGACA CGTGGGCGAC
1551 TTATTGACCA AGTGGGGAGG AAGCAGCCCC GCACTGCTCT CCCGACTGCG
1601 GACCACCGTT GGGCTCATGC GCATCATAAG CCCCACCGCC TCACCTCCAG
1651 TCCCCACAGC GTTCGCGCTC CCAGCCGGGG TAAGCGGAAG AAAACAAAGG
1701 CCGGCTCCA TCAGGGCACC AATCCCCTC GTCCGCCCTT TTCTCGGCCT
1751 CCAATGAGCT TCTAGGGTGT TATCACGCCA GTCTCCTTCC GCGACTGATT
1801 GGCCGGGGTC TTCCTAGTGT GAGCGGCCCT GGCCAATCAG GCGCCCGTCA
1851 GCCCACCCCA CGAGGCCGCA GCTAGCCCCG CTGGCGGCCG AGGCCGGTTG
1901 AAGTGGGCGG AGCGGCGGGC GGGGCGTCGC CGTACTAGGC CTGCCCCCTG
1951 TCCGGCCAGC CCCTCGAAGC ACCTACTCCA CAGGTCCAGC CGGCCGGTGA
2001 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCAGGAGT CCGCCGCCTG
2051 CGCCAGGATG GAGTTCGTGA AATGCCCTTG CCACCCGAA GAGTTCTACA
2101 ACCTGGTGGC CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
2151 GACCAGGTGG GCCGAGCCTC CCTGCTTGCC CGGGGCGGGG AAGGAGCTCG
2201 CTGGGCCGGC CTCAGGGCCT GAGCGGCCGG GCCCAGATCT GGGGCAAGGG
2251 GCGCGGCGAG CAGGGCCGAC GCCTGGGTGT TCCCGTCCCC CTTTCCTCGA
2301 GCCTTCCCCC TGTAGGGCCC GGGTGGACGC GGCCGTCTCG GCTGACCTGT
2351 CCCTGCCCCC GCAAGCCGCC CTGGGCATGA GCGACTTTTG CGTGGTTCCC
2401 GGTGGTTGCG TCCCCGTTT CGTCCCCTCC GTGAGCATCG GCGCTTACCG
2451 GTATTTTAA CCGAGGGTTA CACATCTGAG GCAATGTGGG TGGGTTACGC
2501 GGGAGAGGAC GAGTGAGTTT TTTGGTAAGC GGAATGAACT ATGCAGATAA
2551 CATCACATGA AGGCCGTTTC TGGAATGAAG TCTGACTCCT CCAGTTTCAC
2601 CACCTCTTCC GGAGCTCTCC CCGCCTTGCT GCCTTCCATC GCTTCATCCT
2651 CGGTGCTTCC TGAGTTTTAA AATCGCCTAT CTACGCTTCC AAGTTCCAAT
2701 GAGTTATCTA ACGTCTATGG ATTAGCTAGG TGGTGTTGG AAGGTCAGAA
2751 CTTGGTTTTA CTTAGATTTT TATCTGCCTC ATGCCTGTAC TATTTGTTTA
2801 ATGAATGCAT AGGAGGTGTT TTTATTCCAA CAAGAAAATT ATTCGTACGC
2851 GATTATTGAA TGAATAGACA AATTCAGCCA AGTTCTTCTG GTCTGGACCA
2901 GCCTGGCTGA TTTCTGTAAC TTTTTTGGGC CAACAGGACA GTAGCAAATG
2951 TGA CTAGGC CGAGGCTTGA TAGGTGCCTG AACATCGGAG TCTTCTTTC
3001 AGTGTCATG TGCTTCAGTA AACACACTAG AAAATAAAT TCTGGTTTTT
3051 GTCCCCAGTA GACTACACCC TCATTTGGTG TTATTTTTC CGTGCTATCT
```

FIGURE 3A



3101 TTAATACAGG TACATCCTTC AGTCTATTTG TAGAACATTC AGTTTTCTTC  
3151 ATCTTTTCTT TGCCGGTGCT ACATTATTTG AATTATTTTG CTACAGAATA  
3201 ACTTCTATTA TTTGATATGG CAGATGTCAC TTTTATATAT TAGATATAGC  
3251 ATTCATTTAT TTAACAAATA TTTGACGACC AGTTGTATAT CAGATAGTGT  
3301 TCTAGGTGCT GGAGGTACAA CAGTGAACAA GCTAGGTGAA GACCTTGATT  
3351 TTATAAACT TACTTTTCTAG TGGAAGAGAG ACAATTTAAA AAAGCGAATG  
3401 TACAGTTTTT CACGTGGAGA AAAGCACTGC AGAGGAAGAT ACTAGCAGGG  
3451 CAAGGGATCT GAGTGCAGTC AGACCTCATT TGGGTCCAGA CTTCAATCCT  
3501 CTATGTCTCT TTCCTTTCTA CAGAAAGACT GTTAGAGAAA ATGGTAGCAT  
3551 TGGTTTCTCT TTGGGAGGGA AAGTGGGTGG TCATGGTAAG TGGGTAGAGA  
3601 AAGACTTCAC AGTATACTGT TTTTGTACAT TTTGAGTTT TTTAAAAGCG  
3651 AGACTTGAGC TATTCTAGCT CTGATAATAT GGTGCAGTAT TTGTTATGTT  
3701 AGTTGTAGTC TTTCTGGGCA GTTTTTACAT CCCCATGAGC CGTTAAAAAA  
3751 ATACCTGAAC CTTTAATTAG GGGAAATAAA TTGGAAAAAT ACATTTCCCT  
3801 TCACTTAACA TTACTTTAGT TTCTCTTTT TTTTTTTTT TTTTTTGAGA  
3851 TGGAGTCTTG CTCTGTTACC CAGGCTGGAG TGCAGTGGTG GCGGGACCTC  
3901 AGCTAGATGC AGCCTCCGCC TCCTGGGTTC AAGCAATTCT CCTGCCTCAG  
3951 CCTGCTGAGT AGCTGGGATT ACAGGCACCT GCCACTACGC CCGGCTGATT  
4001 TTTTGGTATT TTTAGTAGAG ACGGGGTTC ACCATGTTGG CGAGGCTGGT  
4051 TTTGAACCTT TGACCTCAAG TGATCTGCTC GCCTTGGTCT CCCAAAGTGC  
4101 TAGGATTACA GCGGTGAGCC ACTGCACCCG GCCTTTTTT TTTTTTTTTT  
4151 GAGGGGGGGG TCTCACTCCA TCGTCCAGCG TAGAATGCTG TGGCCTGAAC  
4201 ATGACTCACT CCAGTTTTGA CTTCTTGGC TGAAGCCATC CTCCCACCTC  
4251 GGCTTCCTGA TCCCGAGTAG CTGGGACTCC AGGCACGTGT CACCAATGCA  
4301 TGGCTAATTT TTAAATTTT TTGTAGACAC AATGTCTCGC TGCATTGCCC  
4351 AGGCTGGTCT TGAACCTCTG AGCTCAAGCG ATTTTCCAC CTCAGCCTTC  
4401 AAAGTGCTGG GATTACAGGT GTGAGCCACT GCACCAACC AGTTTCTCTC  
4451 TGCAAACTAG GGAATAAAT TACGCTTAGC AGATATTGAG GGCTGATTAT  
4501 TTCTATCACA GAAGCATTTG GCTATAGAAT TTCAGGTTT AGTAACTTG  
4551 ATTTACACTG AATTTTTAGG TGCATATCAG TAAATCTACG GGCATATGCC  
4601 GCCTGCAAGT TGTGTGGCAT CACCCAAAAG CCGAGAGTAA TGGAAAGAGC  
4651 AGGCTGTTAG TAATCAGGCA GATCTGGCTC CTGTCCAATC TAAATCCTGT  
4701 TATTTAGACT AATATCTTAA GTCTGTTATT AAGTCCGATT TCTGACGCTA  
4751 TTAAGTTAGG TGAACAACCT TGGTAACTTA ACCTCTGAAC CACAGTTACT  
4801 TCATCTGTAA AATAGGGATG TATGTATGGT AACGATTTT TAACCACAAC  
4851 TTCCCACTC TAAGATGGTC TGAAAAGAAT TTTTGTAGTG TTTGGCTCAG  
4901 AATCACTTGG CAGCAAAACC TGACTTGAAG TTGAGGCTTC ATTCATCCCA  
4951 CTTAGTATAT TCAAATGTTT TGCTAAAGAA ATAATTATGA GGTGCTACTT  
5001 CACACTGACT AGGGTTGTAT ATGCATTTA TTGCCTATTT TCTAAAACAC  
5051 TAAAAATGCT AAATCTGCC CCAGGCTTG CCACAGATGT TTCAGTGGAC  
5101 TATGGCCCTG TGAGACCTTA AAGGGTTGAT TGAGTAAGGA TCACAGGTGA  
5151 TGTCCGCATT GTGCTTGCA TGGAGTTAAG TGCTTGATAA ATGGTGGTTA  
5201 TCAATCTGAT TATGTAAAT TATGTAAAT CAGTTCTCAA GTTTGTGGTT  
5251 TTTTCCCTT CCTGGAGAAA TCTATTCTAT TTTAAAGTGA GGAAGGCTCC  
5301 GTGGAGGGCT GGTAGCTGGT AGCTGTTTAC TTGTGGAACT TTCAGCCTGA  
5351 GGCTGGAGCC CCTTCCTGGG AGTCTGGTCT TGTCGTCTTC CTGACCACCC  
5401 CCACACCTT CCTCTAAAT CCCTCCATCC CTGTTTTTCT CCCGCTTGCG  
5451 AGCTTTTGGG AGTGTGCTGA ATCTCAGACT GCAATAGATA AACCAAGAG  
5501 GGACAGGCAC CAGTAGCCTG AGCTTGCTTT CTCCCCGGC TCATGGGAAT  
5551 CAAGCAGTAG AAATTTTTAG TGAGTGTGTT TTTCCATAGT ATGCTTACTA  
5601 GTTGTGTCTT CCTGTTTTGT TCTTGGTGAT TTGAAGAAAC CTGTTTACAA  
5651 GGTAAGGGAC TGAAACAAAT AGGTGACAGG AAAAAGAGCA GCAGGGGTAC  
5701 GAGCTGGAGG AGTAAGTGGC TTGGCTTGCT CTCTTTCAGA ATGGAGGGCT  
5751 GTATGGAAAG GAGGGTAGT GTTCTTGAAG AGTGTGGGG TTTAAATCTA  
5801 GGGGGACCGT GTCTTGGCAT TGATTGAAAC TCCTGGCTTA ACATCACCCC  
5851 GAAACTGTTA GTTGGACTGA ACATGACATT TGGCAGTGCA GTTAAAAACA  
5901 CTTCTGCTG TAGCCTGGTA ATGGTCAGGC TATGTGAAGA GCTGCTCTGG  
5951 AGCTCAGTCC AGAGCGGTA TTCTGTTTCT TTCACTCTGA AATCCTGCCT  
6001 CTCGATATTT TGAGAAGGAA GGAGTTGGTG AATTGTTTTA AAATCCTCGA  
6051 TGAATGCTT CATTTATTCA TGACACCACT TCTGAATATA TTTATGTGCC  
6101 AGACGCTGAA GTTTACTAAT ATTATGGTGC CCAGTAAATA CTTGTTTTTA  
6151 CTAATATTTT TTATGGCAAT AAAATGACTT TTTAGGATT ATGTGATTTA

FIGURE 3B

Docket No. CL001201DIV  
Application Serial No. 10/644,021  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

6201	AAAGATTGAC	CCTTTTGGCA	AAATACGTAT	TCATGATAGG	AAATATATAC
6251	AACATAGTTC	ACTTAAACCT	CCCACCAGAG	CCCAGGGTTC	ACTGTTACCA
6301	TTCTGAAGTG	ACTGGAATTT	CCTAGAAGTG	GATATGCCAT	ATTTTTTTAA
6351	CCACTCCTAT	TGGATATTTG	TTTTTTATTT	TTTTGAGATG	GGGTCCCACT
6401	CTGCAGTGTA	CAATATCATA	GTTCACTGTA	ACGTGTATCT	CTTGGGCTCA
6451	AGCGATCCTC	CCCACCTCAG	CCTCCCTGAG	TAGCTAGTCT	TCAGTAGCTA
6501	GACTATAGGT	GGGCGCCACC	ACAGCTGGCT	TTTTAAAAAA	TTTTTTATGA
6551	ACACGAGGTC	TCACTATGTT	GCCCAGGCTG	CCCTCAAAC	CCTGGGCTCA
6601	AGTGATTCTC	CCACCTTGGC	CTTCCGAAGT	GCAGGGATTA	TAGGCGTGCG
6651	CCACTGCACC	CGGCCCTGTT	GGATAAATGA	TTCCAGTCTC	TCCCAAAAAG
6701	AACTGTTGTA	AGACTGTGGG	GTGAGGGGAG	GGAAGGGACA	AATAGGAACC
6751	CGCCGTATTT	TCCACTCCCT	GTGGGCCTAA	AACTGCTCTA	AAAAATAGTC
6801	CATGAAAAAA	TACATAGTAC	AAACAGCAAC	TCTTTCTGAT	ATGCTTGCAT
6851	TTAAATCAG	GCTTTTCTC	CCTTTTGGAA	AAACACAGTC	CTTGTTTGCT
6901	TTAGGGAAGA	GTAAAGGTCA	GTGCGCTGCA	TTGCATTAAT	TTCGAAGGGA
6951	AAGATGAGAA	GACATCTTGA	AAGGAATGGC	TGGCTTTCTA	GAGAATAGTA
7001	GAGGCTTAAT	AGGTGTCATA	GAAAAACCAG	GGTTGGACAG	TGGTAGTAAA
7051	ACGGCAAAAC	AGATTTTATT	CAGAAAAACT	ACTGCAGTAA	GAGGAGAGAG
7101	ACCTCGGTAC	AGAAGTCTC	CACTGCGAAT	ACAAAGAAAA	GTAGGAATTG
7151	ATGGCGGGGG	AGCCGGATGT	CAGTGGATGG	AAAATTATTA	CGAGGAAACA
7201	CAGGGGTGTG	CATTCTTGCT	GAAGGCAGGC	CAGAGTTATC	AGACATCACC
7251	TGAGGGATGG	AGGGGGATGT	GGAACCTAAT	CGGCTGTCTA	GGGTGATCAG
7301	ATACTGAAGT	TGGGGGATTC	TGGTCAAATC	AATTTAGCAG	GATTCTTGGT
7351	AAAAGTGGGC	GATGCAAAGA	CAGATGCGTT	GAGTACAAAG	TCCAGGCTTT
7401	ATTGGGAAGA	GGATTTACAG	GGAGCCCGAG	TAGAGTTTGG	TCTAGGGAGA
7451	CTCTGTCACT	GGGAGGACGA	GCGAGCCGCT	CGGAAGTGCG	CTGGGTCTC
7501	TTAGCGGCCA	GTGGGTCTCG	GTGAGAAGGG	CAACAGCGGG	AGGAGGCGCC
7551	GGTGCGGAGC	GGGAGGCCGG	GGGCGGGGCT	GCGGGGCTGC	GGGGCGGGCC
7601	CGTTGTGGGT	CGGCCACGCG	CGTATTCGAG	TAGAGGGCGA	GCCCCGTCCCG
7651	CCTCTCGTCG	GGCGCTTCCC	AGATCTGCTT	GAGTCTATGG	AGGAAAAACT
7701	CCGCGGGGTC	CGCGATTCCC	ATGGCCGCG	CCGCCTGCGG	CACCAAGGCC
7751	ATGGCCCTCT	TCAAGCGCAC	CTTGGTGCTG	AGTCCCGCCG	CGGCGCCAG
7801	GGGCCCCGGC	GCAGGCACCG	CCCCGCGGGG	CTGCTGCTTG	CCTCCTGCCG
7851	CCTGGCCCTG	CAAGGACTGG	CCTCGGGGAG	AGGGCGGCAG	GCTGTGGAGC
7901	CGCCTGCCCC	AGTCCCAGTC	CCACTCCCAC	TCCCCTCCC	ACTCCCCTC
7951	CTGCTCCTCG	ACGTCTCCCA	CCGCCGTGTG	TGTTGTCTGC	CCGCAGGACT
8001	CGCTCAGCAG	CAGCCTGAAA	ACTTGCTACA	AGTATCTCAA	TCAGACCAGT
8051	CGCAGTTTCG	CAGCTGTTAT	CCAGGCGCTG	GATGGGAAAA	TGCGGTGAGT
8101	GATGGAGGCA	GCGCCTCTGG	CTTGGAGGAA	AGCTTGTCCG	GGACTTTTGA
8151	GTGTGTTGGA	AGCTACCTTT	TGATATAGCG	CTCAGCGTTG	CAGCCTCGTT
8201	GCTGTGGCTT	ATCCAGAACA	TAGCCCGGCC	CTACGTGTTT	ACTTTAGAAA
8251	GCCCTTCCAG	GCTCTTTGCC	ATCTAGTAGA	GTCCCTGCGG	GCCCAGCCTT
8301	TCAGAGAAGG	GGGGGGAGGG	GGTGATGTTT	ATTAACTTT	TTTAGTCTTG
8351	GCAGCTGAAC	CTGCCTGTGA	GCAGGTCGTG	TATTTCTCGG	CTTCCCTTAT
8401	CCAACTTTGC	ATTTCTATTT	CTAGCATATT	GGGTTGATTC	TTTTGAAGCT
8451	GCCTCTGTGC	ACATTACACC	CATGAACCTA	GACCAGTTGC	CTTTATGTAT
8501	GATCGTATTT	ATACTGAGAA	GTTACTGTGT	TTTTTGACTT	TCTTTTCTAT
8551	TTGCTACATA	TTAGTTCGGT	CTAAACGTTT	GGTCTTCTGG	TCTCCATAGT
8601	TCTACATTGG	TTAAATGCAA	CTCACTTCTG	GGAGTAGTGG	TGACATTCAA
8651	CTAGTAGGCT	TTTTAATAAA	CTACAGAAGT	TCATTACTCT	CATGTAAGGA
8701	AGGAAAACTA	ATGTAACTTT	CGTTAAGTAT	GAAAAGCGTT	GGATATCCTT
8751	ATAGTTCTTT	AGAGTTAAGG	GTGAGATGGG	TTTAGAAAAGT	GGCCAGGCAC
8801	AAGTTATTTT	AAAATAAAAA	ATCTTTGGCT	GTTTGTTCCT	ATATATTAAT
8851	AGTTTTCCCT	TTTTTACAGC	AACGCAGTGT	GCATATTTTA	TCTGGTTCTC
8901	CGAGCTCTGG	ACACACTGGA	AGATGACATG	ACCATCAGTG	TGGAAAAGAA
8951	GGTCCCGCTG	TTACACAAC	TTCACTCTTT	CCTTTACCAA	CCAGACTGGC
9001	GGTTCATGGA	GAGCAAGGAG	AAGGATCGCC	AGGTGCTGGA	GGACTTCCCA
9051	ACGGTGAGTG	GGGTTACGCA	TCTTGTCTAC	GGACTGTTGT	GTTTCATAAT
9101	GCTAACGTGG	TTGTCCGGTA	GCCTCCATAC	ATGTGGAGAA	AGGTAAATA
9151	AGCATTCTGA	GGGCAGCATA	ATGTGAGGGT	TAAAACTCC	GGTAGCCAAG
9201	ACTCTGAAGC	CAGGCTGCCT	GGGTTGGAAT	CTCAAACTCC	CCACTTACTA
9251	AACTGTTGGT	TACTTACAAA	GACTCTCTGT	GCCTCAGTTT	CTTCATCTGT

FIGURE 3C

9301 AAAATAGGGG TAATAATAAC ACCTACCTCA TGGTATTCTG AGGATTCAAA  
9351 GAATTAACGT AGGTAATGCT CTTAGAAATGT TAGCTACTGC TGTTATTATC  
9401 AGTATTGGAA GTCCAGTGT TCTTCCTGTG GGAAGACGCA GTCAAATTTT  
9451 AGTGTGTGA AAGATTCTCA GGCTAGCTCA CAAAAGCCTG CCGACTGTAT  
9501 GATGCAGCCT ACCTGTAACA CTGCTGGCCT CTTGACTACC CGGAGCCTGG  
9551 TAGCATGGGA CTGCTGCTCA CGATGGGCAG CAGCCTGGCA TGGGGGCGGT  
9601 GTCTGTTGGC AGCTAGGGCG AGCCTCTGCC ACTTCACCTG TGATCCTGGG  
9651 CAAGTTCCTT ATCTGCTTTG TGTCTCCGTC TCCTCGTTTG TAAAGTTAGA  
9701 GCTGAGAGGA TTAATTTTCGC ACATATAAAG TACTTAGTGC CTGGTACAGG  
9751 GTAAGTATTC TGTAAGTATT AGCTATTTGG TCTATTTTGT TGGAGTAAAG  
9801 TGGGTTATAG TTAATAATCCT AAGATTTTAA AAGTCCCTCA AGTTCACGTG  
9851 GACATCTGCC TAGGTCCTAC TATCCTAGAA TTCGCATGTC TTATCACACA  
9901 AATAACTGAT TCTTCCATAT CTTATAAATA AAGGTTTGAT TTAGCAAAGT  
9951 CACATGTTGT GTAATAGCTC GAAGAAGCCC TTTTGTCCA CAGTTGCCAG  
10001 AGCTTTTGGG GAACAGTCCT TATGTTATTG AAACAAACCT AATCTGTAGC  
10051 TGAGTTGGGA GGGAGCTAAG TGGACAGAGA GTCCTCCACC CAAACAAAAG  
10101 AATCTTTGAT TCTTGGGCAT AATGGGAGCA ATATTTAAAA AAAAAAAAAA  
10151 AAAAAAAAAA GGAATGTTTG GGAAGACTC TTGCGGTGCA AAGGCTGTTT  
10201 CAGATTGCTG AGATCAGACC TTAAGTACCA AAGCCCAAAT ATAGTACAAC  
10251 ATAATACAAA TGAGAAGAAA ATAGCTGAAG AATAATTCGA GTTTATACAG  
10301 TACAATTCAA GAGAAGAAAG AAAATTTATG ACGACTAGCT GGGTGAGAAT  
10351 TAGAACTGTA ACCCTGGGAA GGTCCCTGGT ATTTGACTCT CACAGGACAC  
10401 CTGATGACCA GAGGATGGGT TTCCTTTGAT GGGAAATCTG TGGCGATTCA  
10451 TTGATGGGCC TCTGAATTCT GCTGAAGCAG AGGAAGTAGT AATACCCCAT  
10501 TTATAATGGA AGTGCATTCT CACTTAAAAA CAACTAATAT TATTCTAGCT  
10551 GGACCTAGCC TCTAGAAACA GCCAAATTAC ATTTGACTTG AGTGGATTCA  
10601 TAATAATTAA AAAATTTCTG GGGCATGGGA TAAATGTGTT AGGTATTGCT  
10651 AAGTCAAGGC AGCCCTATCC CCTCAGCAGA AGTGAGGGAA TATGAAAGTG  
10701 TGTGAATGCT AACATAAATT TGGGGAATAT CGCCGTCAGA TTTCCAGATG  
10751 ATATTCCAAC ATGTTTGTGA AACTTCAGTG TCTTCCTGTG TTCATACAGT  
10801 GTTCCAGTGG AAAAATAATG CTTAGTTCTG GAAGGTTTCA GATGTGAACA  
10851 CTGAACCTCAT CGTTTTCTTT TTTGGGTAGT AGAGTTAGAG ATTCCATCCT  
10901 CTTGAAAGCA CAGTTGCCCC GGAAGAGTA AAAGGGAGCA GAAGGCGTAA  
10951 GCCAGGCACG GCTGTTTTCA CTGTTGTTCA CCTTTTGTAT CCTTACGAAT  
11001 ATGAAGATGT ACTAAGTTGT GTGTTTTGCG TGCATATATA ATTTTAAGCT  
11051 ACTTGAGTTG TAGGTCCCTC CAGTCTGTGA TTCAGTTTGA GATGGGACTG  
11101 TATGGGAATT AACAGTGCCT TGTCTTCTTA AGCAGTGATT TGTGTATGTG  
11151 CTGATATAGC TCAGTATGTC TTTGAAACCA GTTGTCTGGG GCTAGGCCTG  
11201 CAATCAGCTT TTGGCTAAGA GGTCCCAGGA TGGAACAAGT AGTGTGAAAG  
11251 AGGACTGATA CCTTGGCCTC ACACACAGTA CTGCTCTTAG ACTGGGGCAA  
11301 GTGAACTCC TCACCTCAGA GTGCCCCATT CTAGGCCCCC TCACTCCCAA  
11351 AGGGGTGAGG GATCACTGGG GCCATGGGAA TGTGCTTGT CAGCTCTCGT  
11401 GGGCTCTCCT TCTGTACCAC GTTCTGGACA TCTGGAGTTC CTTGCCCCAA  
11451 ATCCCTGAGC CCACGTCTGC GTCCGCACAG TCTATTTCTT AAGGTCAGTC  
11501 CATCTCCTCC AGGTGGGAAC GTGCCACCAT TGACTGTGCC CTTGGGCCTG  
11551 AGTGATGGCC AAGGGCTGTG TTGGGGAGTG TTGTGGATGG ATCCTGGCAC  
11601 CGAGGGCTGG GATATCCTCT CAAATGAATG TGAGGTGCCT CCCAGTGCTG  
11651 GAGAGAGCGG GATTCAGGAA GCAGTGGAAG GGAAGAGCCT GGGATATGGG  
11701 GATCAGCTGT CTGTGCCCTG CTGCATTCTG GAATAAAACT CTGAGGGACT  
11751 AAGAATTCTA AATTCAAACC TGAATCAACC AGGTGTTTAC AAAGATAAGT  
11801 TTGTCAAGTC AGGAGGATAC AATATATTTT ACTTAAGTTA CTAGCTCGAT  
11851 TGATCATTTT TAAATTTTAA GCTACATATA GTATGTGGGC CTCCATTGTG  
11901 CCTCTTATCC CAGGCCTTGC AGAATTTAGG AATAAGCCTC AATACAGTGT  
11951 TCTAACCAG TGACTTCCGC CTCGATGTAC AGTAGATTGA ACCTGATCCT  
12001 TTATACTTTA GTGATCATTG GTTGATACCA GTTCAAGTCA GGCTTTCTAG  
12051 AAATCTCATT GTATGTTAGG GGTTCGATTA GAGTACAGTC ATGCATCACT  
12101 TAATGAATGG CCACAGGATA CATTCTGAGA AACGCATTGA TAGATGATTT  
12151 CATCATTCTG TGAACATCAT AGAGTGTACT TACACATACC AAGATGGCAT  
12201 AGCTACTACA GACGTAGGCT CTGTGGTACA GGCCATTGCT CCAAGGCTGC  
12251 ACATCTCTAC AGGATGGTAC TGTACTGAAT ACTGTAGGCA ATTGGAGCAC  
12301 AGTGGTAAGT ATTTGTGTAT TTAAACATAG AAAAGGTATA GTAAAAACAG  
12351 GGTGTTACAG TCTTAAGGGC CCACCATTGT ATTTCCAGTC TCCGTTGACT

FIGURE 3D

12401 GAAACATCAT TATACAGTAC ATGAGCACGT ATCTTTCTCA CCTGGTACTA  
12451 GTGGAAAGCT AGAAGGCTTA GAAGTCTACC TGTAACATA GCTTAAGTAA  
12501 TAATACAGCC TTATTTTAA ATGATAATAG CAATAATAGT GTTCACTTAT  
12551 TGAGCATTTT ACTATGAGTT ACTTACTAAA TATATTTTCA CGTTAATTTA  
12601 CTCTTTGTGT TATTTGATCT ATAACATCGT TTAACAGGGA AATTACCTAG  
12651 TACATAATGT ACTGTTATCT ACATTTTATC TAGATGAGGA AACTGAGGCA  
12701 CAGAGAAATT AAGTACTTTG CCTAGGATTA CCCGTGAAGT TAAGTGACAG  
12751 AATCAATGAA TCTGGAAGGT CTGGCTTACC ATCTCTTGTG CTGAGTCACT  
12801 CGCATACTTT ACTACCTCTA AGGTTTCTAA TCAGAGGAAT TTGTATCTGT  
12851 ATTCCCTGCT ACTCTTACCC TCTATGTGGG ATTTGGCCTT TCTCCATTAT  
12901 CCCTGTGAAC TCGCTCTGGG ACCTTCCTTC TTGTACTTGG AACCATCAGA  
12951 AAGTGATCTG AGAACATAGA AATCTACTGT GTTGTGAAAC AGAATTACCT  
13001 GGAAGCGGAA AAAGCCCTCC TGGCTCAATT CACATGTCAC GGCTTATGGT  
13051 CGTATCCGGG GAACATATGA AACTGGGCAC TGAGTGCGGA GTCAGGAAAG  
13101 CCCTGTCCAT TCTGGGGTTC TCTGGGGAAA ACGTGGACCC CTTCAATTGT  
13151 ACTTTCTCCT GTATATTTT GTTTTTACTT TTAGAAGTGT ACAATTACGT  
13201 AATAAATAAT AAAAAGTCGT TGGAAGGATA GGTGAAGTTC AGAAGTGAAA  
13251 GTGTTTTGGA GGAGTCTAAG CTCCTTCCCA CCCTCATTGA CTTTCCTCT  
13301 CTAATAAATA GAAGTGGTCT AACCAAGGAT CTGTGGAATG AGCAGAGTCC  
13351 AACGGAGATT CAGGGATTCT AATAACCTCT TGTAGAATCA CTGGTTTGTT  
13401 TCAGCCACAA GAAGGAATTA CCTTTTGACA TTGGCTTGAA CAGCTGTGT  
13451 GCAAAGAAAA ACTTTTGA AAGTTCTGGA AGTACCAGAT TGATTTTATA  
13501 GGTTTTTTTT TTTTTTTT GAGGGACATG GGGGTATTGA CAGTTGATGT  
13551 TAATCAGAAA TCCTAAATTA TGTGTATTCC TGGTATGTG CAATCAGCCG  
13601 GCCACCTGGT TTTCTCTGG GCTCTTAATT TTAGGTGTAT TCCGAGGAAG  
13651 TTTTCTAAC TTTTCTGTAA ACACAGACCA GGTATATTGC ATACTTCAA  
13701 TGTTTAACCA AATCTCTTCA CTGTTTGCAG TATTATCTGT AGGCTCTCAT  
13751 GTTTTAAAGC TTCCCATGG TGTTTTGTG TTGTATTTG CTAACCTATA  
13801 AACAATCTT TGAACCTAAA ACAAGATATT TGGGCAGTAA CAATAAATTT  
13851 TAAAAACATC AATTCAACTT TTTTACATTA GGGCTTGGAC TATGGAAAAA  
13901 GTATTGGGCA GCATGCCTCA TACTGAGTTG TTTAATGAAT TTTAAAGTAT  
13951 AGCCNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
14951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

FIGURE 3E

Docket No. CL001201DIV  
Application Serial No. 10/644,021  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

15501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
15951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
16951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
17551 NNNNNNNNGT GGAGAGTCT GTAGATGCT GTTAGGTCCT CTTGGTCCAG  
17601 AGCTGAGTTC AAGTCCTGGA TATCCTTGTT AACCTTTTGT CTTGTTGATC  
17651 TATCTAATAT TGACAGTGGG ATGTTAGACT CGCACACAAT AATAATGAGA  
17701 GACTTTAAGT CTTTTTCTAG GTCTCTAAGG ACTTGCTTGA TGAATCTGGG  
17751 TGCTCCTGTA TTGGGTACAT ATATGTTTAA GATAGTTAGC TCTTCTTGTT  
17801 GAATTGATCC CTTTACCATT ATGTAGTGGC CTTCTTTGTC TCTTTTGATC  
17851 TTAGTTGGTT TAAAGTCTGT TTTATTAGAG ACTAGGATTG CATTCCCTGC  
17901 TTTTTTTTTT CGCTTGGTAG ATCTTCCTCC AGCTGTTTAT TTTGAGCCTA  
17951 TGTGCATCTC TGCACGTGAG ACGGCTCTCC TGAATACAGC ACAGTGACGG  
18001 GCCTTGACTG TTTATCCAAT TTGCCAGTCT GCGTCTTTTA ACTGGGGCAT  
18051 TTAGCCCACT TATATTTAAG GTTAATATTG TTATGTTTGA ATTTGATCTG  
18101 TCATTATGAT GTTTGCTGGT TATTTTGCCC ATTAATTGAT GCAGTTTCTT  
18151 CCTAGCCTCG ATGGTCTTTA CAATTTGGCA TGTTTTTGCA GTGGCTGGTA  
18201 CCAGTTGTTT CTTTCCATT TTTACTGCTT CTTCAGGAGC TCTTTTAGGG  
18251 CAGGCCTGGT GGTGACAAAA TCTCTGAGCA TTTGCTTGTC TGTGAAGGAT  
18301 TTTATTTCTC CTTCACTTGT GAACTTAGT TTGGCTGGTT ATGAGATTCT  
18351 GGGTTGAAAA TTCTTTAAGA ATGCTGAATA TTGGCCCCA CTCTCTTCTG  
18401 GCTTGTAGGG TTTCTGCTGA GAGATCTGCT GTTAGTCTGA TGGGCTTCCC  
18451 TTTGTGGGTA ACCCGACCTT TCTCTCTGGC AGCCCTTAAC ATTTTTTCTT  
18501 TCATTTCAAC GTTGGTGAAT CTGACAATA CGTATCTTGG GATTGCGCTT  
18551 CTCGAGGAAT GTCTTTGTGG TGTCTCTGTT ATTTCTTGAA TTTGAATGTT

FIGURE 3F

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18601 GACCTGCCTT GCTAGGTTGG GGAAGTTCTC CTGGATAATA TACTGAAGAG
18651 TGTTTTGTAA CTTGGTTCCA TTCTGTCTAT CACTTTCAGG TACAACAATC
18701 ATAGCATTGG TCTTTTCACA TAGTCGCATA TTTATTGAAG CCTTTGTTCA
18751 TTTCTTTTCA TTCTTTTTTC TCTAATCTTG TCTTCTTGCT TTATTTTCATT
18801 AATTTGATCT TCGATCACTG ATATCCTTTC TTCTGCTTGA TCGAATCGGC
18851 TATTGAAGCT TGTTTATGCT TTGTGAAATT CTTGTACTTT GGTTTTCAGC
18901 TCCATCAGGT CATTTAAGCT CTTCTCTACA CTGGTTATTC TAGTTAGCCA
18951 TTTGTCCAAC CTTTTCTCAA GGTTTTAAGT TTCCTTGCGA TGGGTCAGAA
19001 CGTGCTGCTT TAGCTTGAG AGTTTTGTTA TTACCAACCT TCTGAAGCCT
19051 ACTTCTGTCA ACTCGTTAAA CTCATTGTCC ATCCAGTTTT GTTCCTTTGC
19101 TGGTGAGGAG TTACGTTCCCT TTGGAGGAGA AGAGGCGTTC TGTTTTTGGA
19151 ATTTTCAGCC TTTCTGCTGT GGTTTCTCCC CATCTTGTG GTTTTATCTA
19201 CCTTTGGTCT TTGATTTTGG TGACGTACAG ATGGGTTTTG GTGTGGGTGT
19251 CCTTTTGTG GATATTGATC CTATTCCTTT GTTTGTTAGT TTTCCTTCTA
19301 ACAGAGGCCC GTCAGCTGCA GGTCTGTTGG AGTTGCTGGA GGTCCACTCT
19351 AGACCTGCTT TACCTGGTA TCACCAGTGG AGGCTGCAGA ACAGCAAATA
19401 TCGCGGCCTG ATCCTTCCCTC TGGAAGCTTC GTCCAAGAAG GACACCCACC
19451 TATATGAGGT GTCTGTCGGC CCCTACTGGG AGGTGTCTCC TCCCAGTCAG
19501 GCTACATGGG GCTCAGGGAC CCACCTGAGG AGGCAGTCTG TCCGTTACTG
19551 GAGTTCAAAT GCCGAGCTGG GAGAACCACT GCTCTCTTCA GAGCTGTCAG
19601 GCAGGGATGT TTAAATCTGC AGAAGCCGTC TGCTGCCTTT TGTTTAGATA
19651 TGCCCTGCC CACAGATGC AATCTAGAGA GGCAGTAGGC CTTCGCGTGG
19701 GCTCCACCCA GTTCAAGCTT CTTGCTGCT TTGTTTACAC TGTGAGCATA
19751 GAAGTGCCTA CTGAAGCCTC AGCAATGGCG GGGAGGCGCT TCCCCTCACC
19801 AAGCTCCAGC ATCCCAGCTT GATCTCAGAC TGCTTGCTA GCAGCAAGCA
19851 AGGTTCCATG GGCATGGGAC CCCCCGAGCC AGGCATGGA GGCAATCACC
19901 TGCTCTGCCA GTTGCGAAGA CTGGGAAAAG CACAGTATTT GGGCAGAGTA
19951 TACTGTTTCT CCAGGTACAG TCACTCACGC CTTTCCTTGG CTAGGAAAGG
20001 GAAATCCCCT GACCCCTTGC ACTTCCTGGA TGAGGTGACG TCCTGCCCTG
20051 CTTTGGCTCA CCCTCCATGG GCTGCACCCA CTGTCCAACC AGTGCCAATG
20101 AGATGAACCA GGTACCTCAG TTGGAAATGC AGAAATCACC CATCTTCTGC
20151 ATCGATCTTG CTGGGAGCTG TAGACCAGAG CTGTTCTTAC TGGGGCATCT
20201 TGGAAGCAAC TCTGGGCTG AGTTTCTGTT TGTTGCCCTG ATGTATATCC
20251 CCAGTGCCTA GAATGATACT TGTTACATAG GAAGTGCTTG ATCCATGTTT
20301 GCACAAATGA ATCTTTCTCA TAATGAGGTT TCTCTAAACA AGCTGTTCTC
20351 CCAAAAACCT ACACCCAGCT TTATGTTGAA GCATCTCATT ATACATTGGA
20401 AAGATGAAAT GTGTAGTGAG ACTTTGAATC TTCTTTTGAA TCTAGAAACA
20451 TTAGCATTTT TAGACCATTC TATTTTAATA TTTATGAAAT TTATGAAATA
20501 ATAAGAAACA TGAGGCCGGG CTCAGTGGCT TATGCCTGTA ATCCCAGCAG
20551 TTTGGGAGGC CAGGGCTAGT GGATCATGAG GTCAGGAATT TGAGACCAGC
20601 TTGGCCAACA TGGTGAAACC CCACTTCTAC TAAAAATATA AAAATTAGCT
20651 GGGCGTGGT GTGCATGCCG GTAATGCCAG CTCCTGGAGA GGCTGAGGCA
20701 GGAGAATCAT TTGAACCTGG GAGGCGGAGT TTGCAGTGAG CTGAGATCGT
20751 GCCATTGCAC TCCAGCCTGG GCAACATTGC GAGACTCCAT CTCAAAAACA
20801 AAAACAAAAA CAAAAAAAT GTGTGACCTA AATTAGGCTT ATAGATGAAC
20851 CATTGCAGTC ATGATTAATT CCGCCATTGT TTGCCTTGTG ATCTTTGTG
20901 CCATGTCTGT ACATATTTCA TGATTTCTGT GTTTTACGG TTTCATTTC
20951 AGATCTCCCT TGAGTTTGA AATCTGGCTG AGAAATACCA AACAGTGATT
21001 GCGACATT GCGGAGAAT GGGCATTGGG ATGGCAGAGT TTTTGATAA
21051 GCATGTGACC TCTGAACAGG AGTGGGACAA GGTTAGTCTC ATAAAACAGT
21101 GTCTGTGTGT GATGTATTAG ACAGAGCTGG CAGTCTCAT AGTGAAGCTC
21151 AGAACAAGAA AAGTTGTCCA GTATTTTCTG CCCCTCTGGT TTTACAATTC
21201 ATCTGTTTAG GTTGAATGTC TCATCATAAA CAGTTTATTC CAGAGTTAAT
21251 TCCAAACCAG CAGCTATGTA GGATATCAGC CAGGCTAGGA GTAGGGTACT
21301 GGAGAGAAGT CTTATCTAG ACAAGGGAT GTAATTGACC ATGAAGATTA
21351 AAATAACATA TCAAAACATA AGGTAGGGTT AGGAGTCTTG CCTATTTTTC
21401 ATAGGAATGG TGTTTGTGAG ACTTACTCAT CACTTCTGTG GAAGTAAAGA
21451 CATTTTATTT ATTTATTTTA AAGCCAGTCA GATTTAGCAG GCAGAGACAT
21501 TTCAGACATC TAAAGTGTG ATGTATTTCA TACCTTAAAC TGTGCTTAAA
21551 TTAGGATCTC CGAAAAGATG CTGCTACATG GTCACTACGT TAGTGTAGGT
21601 CCAAGTCTT GGGCCTCTTA ATTTTTCAAA CCTCAAACT TGACAGCAGT
21651 TATCTTTGGA ACTGCTGATT TGTGCTTCCT AAGTTAACAG CATACAATGA

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FIGURE 3G

Docket No. CL001201DIV  
Application Serial No. 10/644,021  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

21701	CTGCTAGAAA	TCAATTTCTG	CATTTAAGGT	GAAGTTAGCC	GGGTACTATG
21751	GTTTACCTGT	AATCTCAGCA	CTTTGGGAGG	CTGAGGTGGG	AGGATCATTT
21801	GAGCCCAGGA	GTTAGACACA	AGCCTAAGCA	ACATAGCGAG	ACCCCGTCTT
21851	TCAAAAAATT	AAAAAATGAG	CAGGGAATTG	GTGGCATGTG	CCTGTGGTCC
21901	CCAGCTACTC	TGGAGGCTGA	GGTGTGGGAG	GATTGCTTGA	GCCCAAGAGT
21951	TGAAGGTGTC	AGTGAGCCAT	GATTGTGCCA	CTGCACTCCA	ACGTGGGTGA
22001	CAGAGCAAGA	CACCTACTGA	AAGAAAATAA	AGTTGAAGTT	AAAACCTCTG
22051	GCCAAGAACC	AGCACTGGTT	ATGATAGTAA	CTCATTTTCT	GTTGTGCAGA
22101	TTTATTCAGG	AACTTAATT	TTAGGTTGTT	GAATAGAAGT	TTTGATCAGA
22151	TAAAAATTGAA	TTAAAAAAA	TTTTTTTTGA	GACAGGTCT	TGCTGTTATC
22201	CAGGCTGGTG	TGTAGTGGTG	TGATCACGGC	TCCCCGCAGC	CTCAACCTCC
22251	TGGGCTCAGG	TGATCCTCCC	ACCTCAGCCT	ACCGAGTAGC	TGTAACTACA
22301	GTGCATGACA	CCATACCAGG	CTCATTTTGT	TACATTTTGT	GTAGAGAGAG
22351	GGTTTTGCCA	TGTTGCCCCAG	GCTAGTCTCA	AACTCCTGGC	ATCAAACAGT
22401	CCTCCCCTCT	TGGCCTCTCA	AATGTTGGGA	TTACAGGCAT	GACCAGCCAA
22451	TTATTTCAAG	GAGTTATTTT	TTTTCTTCTA	CTTTGGGGGA	AGATGAATTA
22501	TATAAGTCTC	CATTTTAGGA	GTATTTCTAC	CAAAAGAACT	ATTATCTTCA
22551	AATATATTTT	TGGATAGTAC	TATAGATATA	CTAATTTTGT	TTTAAATTTC
22601	TAGTAATCTT	TTTGAAGATT	TTGTATAGCT	GTCCAAAGCC	AATTTCTGTC
22651	TACCTAATTT	CAGCAAGATT	TCACTCTTTT	CATGTTACTT	TTGTCCCAGA
22701	ACAAATTTCA	AGTGCTTTCT	CTTCACCTGT	GCATTCTTCC	CCCTGATTAG
22751	TCTCTGGCTT	TGTATTACTT	TCAGTCAGAG	ACGACTTTT	TTTTTTGAGA
22801	CAGGCTCTCA	CTCTGTCAAC	CAGACTGGAA	TGCAGTGGCA	CAGACAAGGC
22851	AGCCTTGACC	TTCTGGGCTC	AAGCAATCTT	CCTTGCCCTC	AGCCTCCTGA
22901	GTAAGTGGGA	CCACAGGCAC	GTTGCCACCA	TGCCTGGCTA	ATTTATTTTA
22951	ATTTTTATTA	TTTTTGAGAC	AGGGTATTGC	TCTGTCACCC	AGGCTGGAGT
23001	GTAGTGGCAT	GATCAAGGCT	CACTGCAGCC	TTACCTCCT	GTGCTCAAGC
23051	AGTCCTCTCA	CCTCAGCCTC	CCCATTAGCT	GGGACTATAG	GTCCACACCA
23101	CTACACCAGG	CTAATTTTGT	TAATTTTTTG	GTAGAGACAG	GGTTTCATCG
23151	TGTTGCCTAG	GCTGGTCTTG	AGCTCCTGGG	CTCAAGCGAT	TCACCTGCCT
23201	TAGCCTCCCA	GGTGTGAGCC	ACTACACTCA	GCCTTTTAAA	ATTTTTTACA
23251	GAGATGAGGT	CTTGCTTTGT	TGGCCAGGCT	GGTCTAAAAC	TCTTGGGCTC
23301	AAGCAGTCCC	CTCTCCACAG	CCTCCCAAAA	TTCCGGGATT	ACAGGCGTGA
23351	ACTTCGGTCA	TTTCCTAACT	TTTACCCTTC	CTAATGACAC	TCCAGAGCTT
23401	ACCTTCTTTA	CTTTTGCTTC	TTAAGTTAAC	TAATAGACAA	TTATTGTATG
23451	TGGATATTGC	ATTAAGTTGT	CTTAGGATAC	CCTTTTCAGA	GGAGGACAGC
23501	TTTTGACAAA	TTGCTGTCGC	GGAAAAAAA	AGTATTTGGC	AATTAAGAGT
23551	TGCATTTACT	GAAATCTCTG	TTGAGAGAGG	GGAAGTTACG	TTGTCTCTAA
23601	AAGAAAAACT	AAAAAGAAAA	GGGGAAGTTT	TAGCAAAGTT	GTTAAAGCCT
23651	GACACTTAAG	TCATACTACC	TAGTTTTGAA	CTCTTAGCCC	CTGCCACAGA
23701	CACGGCAGCC	CCTTGAACCT	TCCTGGGTTT	AAGCGAGCCT	CCTACTTCAG
23751	CCCCCTGAGT	AACTGGGACC	ACTGGCCTGT	GTCAGTGTGC	CTGGCTAATT
23801	TTTTTTTTTT	CCTCACATGG	GCAATGTTGG	GCAAGTTAAA	TCGACTTCTT
23851	TGTGCCTCAG	TTTCCTCATC	TGAAATGGAG	ATCATACTGC	TATGTACCTG
23901	ATACAATGTT	TGTGAGGATT	GAATGTGCAG	AGTTCTTTT	TTCTGTTGTT
23951	GTTGTTTTGA	GACGGAGTCT	CACTCTGNNN	NNNNNNNNNN	NNNNNNNNNN
24001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
24051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNA	TCTCGTGATC
24101	CGCCCGTCTC	AGCTTCCCAA	AGTGCTGGGA	TTACAGGCAT	GAGCCATCGT
24151	GCCCGGCTGA	ATGTGCAGAG	TTCTTAAAAC	CGTGTCAAGA	ACATAAAATA
24201	GTTATTTGTT	CTTTCATATA	ATGATGATTT	TGAGGGCCTG	CGGATCTTGA
24251	CATGTTATCA	GATTGGTCAA	AAAAAGATTA	AACCATAGTT	GGTATTGTCC
24301	TAGTTCCTGT	TACCAGAATA	TTCCATCTTT	CATCGTTGCC	TTCTCTCATA
24351	GTTTTATGTA	TCAAAAAGTT	TATTGTAAAG	CTAGGCCGGG	CACGGTGTCT
24401	TGGGCTGGTA	ATCCCAGCAC	TTTGGGAGGC	CAAGGCTGGC	AGATCAGTTG
24451	AGGTCAAGGAG	TTTCGAGACCA	GCGTGGCCAA	CATGGTGAAA	CCCCGTCTCT
24501	ACTAAAAATA	AAAAATTAGC	TGGATGTGGT	GGTGGGTGCT	TTAATTCCAG
24551	CTACTCAGGA	AGCTGAGGCA	GGAGAATCAC	TTGAACCCAA	GAGGCAGAGG
24601	TTGCAGTGAG	TTGAGATTGT	GCCACTGCAC	TCCAGCCAG	GGGACAAAGT
24651	GAGACTTGAT	CTCAAAAAAA	AAAAAAAAAA	AAAGTTATTG	TAAAGCTAGA
24701	CACGGTGGTA	TTTGCCTACA	ATCCCAGCTG	TTCCGGAAGC	TGAGGCAGAA
24751	AGATTGCTTG	GGTCCAGTAG	TTTGAGTCTA	ACGTGGGCAA	ATATATGAGA

FIGURE 3H

24801 CTCCATCTCA AAAAAAAAAA TAAAAAATAA AAATAAAAAA ATGTTTACTA  
24851 GTTTTTTTCA GTAGCCTTTT ATTATAGTAG CAGTACATGT GTATTGTAGA  
24901 AATTTGGAAA ATACAAGTGA AAAATAAAAA CATCAAATTC CCGTCAGCCA  
24951 GAGACTGCTG TGAAATGTTT TGAGCACATC CTTCTTGAAT GTTTTTTAAA  
25001 TCCTGGTATG TATATTTGTA TTTTAAAAATC AAAATGCATT CTTACCCATT  
25051 CTCTTTTGAA CCTGCTTTT TGTAGCTAAT GATCTCTAGT GTGTCCATTT  
25101 CAGTAAAAAT TCCATTATTA AAGTGCCTTA AAAATCGTCT CTTACAGTAC  
25151 TGCCACTATG TTGCTGGGCT GGTCCGAATT GGCCTTTCCC GTCTTTTCTC  
25201 AGCCTCAGAG TTTGAAGACC CCTTAGTTGG TGAAGATACA GAACGTGCCA  
25251 ACTCTATGGG CCTGTTTCTG CAGAAAACAA ACATCATCCG TGACTATCTG  
25301 GAAGACCAGC AAGGAGGAAG AGAGTTCTGG CCTCAAGAGG TAACAGATTC  
25351 AGGGTATTTT GGGGAAAAT AACTTTAGAC ATTCTCTGAA AAATCCTTTA  
25401 ACTCTTGTGG TTGCGGGTGA CAGAAAAACA AGCCAGGCCT CCCCCAGGCA  
25451 GCATAAGGGG ATGTGGAATA TAGGATAGAT TGACATGAGT TTGCTTCAGG  
25501 TAGACTGGCT GACTCCAGG ATTCACACCA CGTAATCAGT ATATTCAAGC  
25551 CTTGCTGTCC TTGATTTCTT TCAGACGGTC TTTCTCCAAG TGGTGGATAT  
25601 GGTAACAACC CACGTGCACT AGCTTAACAA AAAGTTCTTA GGAATGGCTT  
25651 TGTTCCGGCT GCGCAGTGG CTCATGCCTG TAATCCCAAC AGTTTGAGAG  
25701 GCCAAGGTGG GCGGATCACC TGAGGCCAGG AGTTCGAGAC CAGCCTGGCC  
25751 AACATAGTGA AACCCTGTGT TTTACTAAAA ATACAAAAAT TAGCCGGGCG  
25801 TGGTGGCAAG GGCTTGTAA CCCAGCTACC TGGGAGGCTG AGGCAGGAGA  
25851 ATCGCTTGAA CCGAGGAAGC AGAGATTGCG GTGAGCTCAG ATTGTGCCAC  
25901 TGCACTCCAG CCTGGGCGAC AGAGTGAGAC TCCCTCTCAA AAGAAGAGGA  
25951 AGGGCTTGGT TCTTCTGCTC AGCCCTGAAT CAGTTACTGT TGCTACACAG  
26001 CTGAGTTCTC TGGCCTCACC TGGATTACGT CTACACAGTA CACACAGAAT  
26051 GGATTTCCCC CAAAGAAAGA ATTCTGCGGC AGGAAGGGGA AAGGGATGGC  
26101 AGGTAGACAA AAATCCAGG TGTCTGTAAT AAGGGACAGG GTCGATCTTT  
26151 AATTAAAACA TGGACAGGGA ACAGAAAGCT TTTGATACTG ATTTTGTTC  
26201 GAAGGAAAGT AGAAAAATTT ATGACTGTCT CCTGAATTTA TTCCAGCATT  
26251 TACCTTTTGC TTTCCATAAA AGTGTTCCT GCAGCCAAGT ACTTTAAAGT  
26301 TTTAAAAAGA CGGGTGAGGC TAAGTGTGGT GTCTCATACT TATAATCCCA  
26351 GTGCTGAGGC CAGGAGTTCA AGACCAGCCT GAGCAACACA GCAAGATACC  
26401 ATCTCTATAA AAAATTGTTA GAAAATGATT CTGCTGAAAG AGCAAAAATA  
26451 AAAATTAAAG AAAGTAGAAA AAATAAAACT AAATTTAAAA GATTAAGTGG  
26501 GCATGTTGGC ATGCACCTGT ATTCCTAGGT ATTCGGGAGG CTAAGGCACA  
26551 AGGATCCCTT GAGCGCAGGA GCTCAAGGTT GGATTGAGTT GTAATCACAC  
26601 CACTGCACTC CAGCCTCGGT GGCACAATGA AACTGTCTCA AGAAAAAATA  
26651 AAAGTGACAG AGGGAAACAA TATTTGCAAT TCATAGAGCA GATACAGGGT  
26701 TCATATTCCT AATATTAAAA AAAACTTCTA AAAGTTAAGA AAAAGGCCAA  
26751 CTGCCCCACA GAAAAATGGG CAAGGAGATA AGAACAAGAT TGTTACACAG  
26801 AAGAGACACA CAGATGATTA TTAATAATCT GAAAAGATGC TGAGTCTTAC  
26851 TCCTAAGAAA AATTACATT TAACTACTC TGGGGGCTGG GCAAGGTGGC  
26901 TCACGCCTGT AATCTCAACA CTGGGAGACC AAGGCAGGAA GATCACTGAA  
26951 GCCAGGGTAT CGAGACCAGC CTGGACAACG TAGTGAGACC TTATCTCTTA  
27001 AAACAAAACA AAACAAAACA AAACAAAAAA AACAGTAAAA ATTGGCCGGG  
27051 CACAGTGACT CCTGCCTATA ATCCCAGCAC TTTGGGAAGC CCAGGTGAGT  
27101 GGATCACTTG AGGTCAAGTG TTTGAGACA GCCTGGCCAA CATGGCAAAA  
27151 TTCCGTCTCT ACTAAAATTA CAAAAATTAG CCAAGTGTGG TGGCATACGC  
27201 TGGTAGGGCC AGCTACTTGG GAGGCTGATG TGAGACTCCA TTTAAAAAAA  
27251 AAAAATCAAA AATTAGCTGG GTATAGTGGC ACACCCCTAT AGTTCTCGCT  
27301 CTTGGGAGG TTGAGGCAGG AGGATTGCCT GAGCCCAGGA GTTCAAGGCT  
27351 GCAGTGAACC ATGATCACAC CACTGCATTC TAGCAGCTG GGAGACAGAG  
27401 CAAAACCTT GTCTCAAAAC AAACAAACAA CAACAAAAAC AAAAAACACT  
27451 TCCCTCAGCT CAGACATGGC CTTTAAAGTT TCCTAGGTGA CTCGTGTGCA  
27501 GCCAGGGTGG AGAAACCACT CTTGTCTTAC CCCTCTTTG CAGACACAGG  
27551 GCTCAGAGAA GGGAAGGGGA TTGTCTGGGG ATGTATAGTG AGGCAGTGGC  
27601 TGCCTTGGAA GTGGAGTCTC AGTCTCCCGG CTCCTAGGCC AGCCCCTGAC  
27651 CACTGTTCCA TTGTCTCCCA GACAGAACAT CAGCCACGGG CATGTGATGC  
27701 ATGAGCGTGA GCCACACCAT CTTGCACACA CAGGAGCAGA GCCCTGCTCT  
27751 TCTCATTCAC TTACTTTATC TGTAATAATAG CATCATTTCT ACCACACGGT  
27801 GGTGGTGTGA ATAAATGAG ATGAACCTCT AGCATAGAGT GCTTAGTAAA  
27851 GGTCTGGAC ATTTCTAGT AGTTGAATCA TGCCAAATGT GGTCTAGGT

FIGURE 3I



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27901 GATTGGCTTC TTTTGCTAGC ATGTTTTTCAG GGCTCCTCCA TGCTGGGGCA
27951 TTGCATCACT GCTTTATTCC TTTTATATCGC CTAGTATTAT TCCACTGTGT
28001 GGATAGACCA CATTATATCCA TTCATCAGTT GGAGGATATT TGGGTTCTTC
28051 CCATTTTTTTT TGGCTATGGT GAATAGTACT GTGTACATTT GCATATAAGG
28101 TTTTGTGTAG ATGTGTGTTT TCCTTTTTTCT TGGGTCTATG CTGAGAAGTG
28151 GAATTGCTGG TTCATACAGC AGCTCGAACC TTGTGAGGAG CTGCCAGACC
28201 CTTTTCCAAG GTCGCTCCAC CATTTTACAT TCCCGTCAGC AGTGTGAGAG
28251 TCCCAGTTTC ACCAGCACTT GTTGTTATCT CTTTTTAACT GTATGTATAT
28301 ATACTTAACA TTTTATTTAT AATAAATGTA CATAATAGAG AATTTGCCAT
28351 TTAACTATT TTTAAGTCTA TTATTCAGTG GCATTAAAGTA CATTAAATGAT
28401 GTTATATAAC CATCAACACT ATGTTTCCAG AACTTTTCGCT AGCTTCAGAG
28451 AATCCTCTAA ATAATATCAT TAAAAATCAT CAAGCCGAAT CCCACTGTTA
28501 GAATTAAAGG TTTTATTTCA CTTTCAAGTT ATCAGGATCC AGGGAGGTGT
28551 AATACACTTA GAGGATAGAC TCAGCTCATT TCCCAGCTAT GCCTTTCAGC
28601 AGCATCTTTA CCAGAGTAGG AATATAATGT TAGTCATTAT TTAGAGGCCT
28651 GGCCATCTTG AGAAGGTTTA CTGTTTAGTC TGCAGTACAA TTATAACTGT
28701 TTTTGTATAT TGGGTTATTT TTTTCAGAAG TAGGCCAGTA GCTCTAACAG
28751 GAGCCTCTTT AGCCTGAATT CGTCCAAGTA GTGCAGTGT GCAC TAGTTG
28801 TCCCTCGGGA CATGCTCCCC AATACGTAAC TCACTTCCAG GTTGCAACTG
28851 GACACTTACT GGTAAGTACA AATAGCTATT GCATGGAGCT TAAAATGAAC
28901 TTGATCTTCG TGAAAGATGA GTCTGCAGCT AAGAGACTTT ACTGTATATC
28951 ATAGTGTTTT TTTTGTTTTT GTTTTGTTTT TGTTTTTGTG ACGGAGTCTC
29001 ACTCTTTCAC CCAGGCTGGA GTGCAATGGC GAGATCTTGA CTCACTGCAA
29051 CCTCCGCCCC CTAGGTTCAA GCAATTCTTC TGTCTCAGC TCCTGAGTAG
29101 CTGGGATTAC AGGCGCCTGC CACCGTACCC GGCTAGTTTT TGTATTTTAA
29151 GTAGACACAG GGTTTCACCA CCTTGGCCAG GCTGGTCTTG AACTCCTGAC
29201 CTCGTGATCC ACCCTCCTCG GCCTCCCAA GTGCTGGGAT TACAGGCGTG
29251 AGCCACGGCG CCCAGCCTGT ATCATAGTTC TTATGCACA AGACCCTTA
29301 ATATTGTTTT TAAATTCTCC CCTATGCACA CGCTGACCTG TTCCTTAATC
29351 TTCTTATCTG TCTAGGTTTG GAGCAGGTAT GTTAAGAAGT TAGGGGATTT
29401 TGCTAAGCCG GAGAATATTG ACTTGGCCGT GCAGTGCCTG AATGAACTTA
29451 TAACCAATGC ACTGCACCAC ATCCCAGATG TCATCACCTA CCTTTCGAGA
29501 CTCAGAAACC AGAGTGTGTT TAACTTCTGT GCTATTCCAC AGGTAGGGAA
29551 CGGGGCTCCT CTGGGTGGAT ACGGGGCTAA AGGGAGTGGG GTAGGAGTAA
29601 GGGTGGATTT TGCTGTGCTA TATTCAAGGA TATGATTCCT TAAAAAGACG
29651 ATGACTCCAG TTTATTACGC TGGGAGTTTC ATAGCACCCG CCTTTGCTTC
29701 CAGCCACCAA ACTCAGCTCA GCCTTGAGGT TAAGCCTGCT CCTTTTCAGA
29751 ACCTTCTTTC CGGATTTACT ATTTTCTACA GCTATCCTAA ACTAGTTAGG
29801 TTCTTTTCTT CACAGTTAAG TCAAGGTCTT TGGCTTAGAT TTATGGGAG
29851 TGCTGGGTAA AACCTGGGTG AAGCTGTTAT CATTAAAAAG TCTTCATTAA
29901 GCACCTAATT ACTGTGTCTC TTTTCCTAGA CCCGGCATAA AAAGAACCTG
29951 GTCCGGTAGA CCTAGCCTCT CAGTATGCTA GGAACCTACA CTTTTTAGTT
30001 GCCTTTACCA AGTATTGCAG ATACTACTGC AAATAAGTGA AGAAAGTAAC
30051 AGCATTTAAC TGATTTGGGA ACTTGGTTTG ATCTTGTCTT AATGACCCAC
30101 TTCGAATGGT GGTTGAAAGT AAAATCTGTA TCGCCGTCTT ATGTTTCCAT
30151 TTACCTAGAA ATACTTTACC TTTGAGCACA GGAAATTAAT CCCCTTCTGG
30201 TTGTTCTCCC CCTGGCATTG GTTTTAAATA TATAATGATT ATGTTTGTG
30251 TAGGAAAAAT AGAAAAACAA CTACAATAGA AAATTCTTCC CATATATTAT
30301 TTTGAAATAC ATATTTCCGA TCCGATAATC CATTGCTCTA GCATGGAAAA
30351 TGTTGGATTT ACTTGTGTTT GCTTTTTCCA AATAAAATGG AACTTTTGTG
30401 GCTACATTAT AGAATTGTTT TAGACTGCTT AATTCTGTGT GTTGTGAGA
30451 AAGGGAGGAG TGGGGAAGGT AAAAATCTTG ACATACTTTC TTCGTGGGTA
30501 TTTTTTCTTG AGCGATTCCA TCTTAGTTGA TTAGCAGTTA GCAATTGCCC
30551 ATTCAACAGA AGGTTTTCTT ACCTTTTTGT GATAATGATA GCTAACGACA
30601 TCATTTCTTC TTTTTTCCCT CTCTTCTTGT TGTCTCTAGG TGATGGCCAT
30651 TGCCACTTTG GCTGCCTGTT ATAATAACCA GCAGGTGTTC AAAGGGGCAG
30701 TGAAGATTCG GAAAGGGCAA GCAGTGACCC TGATGATGGA TGCCACCAAT
30751 ATGCCAGCTG TCAAAGCCAT CATATATCAG TATATGGAAG AGGTGGGTTT
30801 TTATTTAACT ACTTGATAA TTTGTAGCTA CTTTTATGAT TTAGTAATGT
30851 CACTGTTTAA CCAGGTTTGG ATATTAGATG ATCCTAACAA TTCACTATCC
30901 TGTGGCCTAA AGAGACGGA ATTGATATCC TTTATAAGGA AAAAAGTCTA
30951 TTCACAGGAG CCGAGCAGAT TGCTCACTGC TGTGTAGTAC CCTGGTGAGA

```

FIGURE 3J

31001 GGAGATAAAAT GGAGCAAGGC TGTAGGTTGG AGCCCCTCAG TAGAATCATA  
31051 GATTTTGGAGC TGCAAGATGA TGCAGGAGGC CAACCAAGCT TCTTGTGCT  
31101 GGTGAGGAAT GTGAGGTTGA AGCTTGTCTG TGCTGATGCA GTGCGTGATT  
31151 GAGTGGATCT CTGGCTCCCG TCCATGTGTC CTGACACCCA GTCTGGTACT  
31201 TTCATTATGC CACAGGCTC AATTGAAAAA TCACAGTAGG GAATTTAGGC  
31251 CAAGGAAAGC CATCAAGTTG CAATTATTTC CTAAATTTTC TTTGGAAAAAT  
31301 TTCATTTCAA ATACCAAAAC CATCCTATAA AAAGAAAACT TACCTTCTTA  
31351 GGTCAAATCT CTAATATTG ACTAGGTTCA AAAAGTTTAT TTCTGGCCAG  
31401 GCACAGTAGC TTACTCCTGA AATCCCAGCA CTTTGGGAGA CCAAGGTGGG  
31451 AGGATCACTT GAGGCCAGGA ATTCAAGACC AGCCCGGGCG ACATAGCAAG  
31501 ACCCCATTTC TACAAAAAAT TTA AAAAATG TCATGGTGGT GCACGCCTGT  
31551 GGTCCCAGCT ACTCAGGAGG CTGAGGCAGG TGGATCACAT GAGCCTGAGA  
31601 GGTCGAGGCT ACAGTAAGCT GTGTGATTTC ATCATTGCAC TCTAGCCTGG  
31651 GTGATAGAGT GAGACTTTGT CTCAAAAAA AAAAAAAAAA AAAAAGTCTT  
31701 AGAGACAGA AGTCTCTGA ATCTCTAATA ATCTCTAGGC CCTAGAGCAG  
31751 TGGTTTGTAA ATGGAGTGA TTTGCTCCCC TCCCCCAGA GGACATTGGA  
31801 CAATGTCTGG AGACATTTT GATTGTCTTA ACCGGCAGGA ATCGGGTGCT  
31851 ACTGGCATCT GGTGAGTAGA GGCCAGGAT GATGCTGTGA TCCTCAGGTG  
31901 TGATCCTGTT GAGAATGAAA CACTGTAGAC TTTATGAAA CATACAAGAC  
31951 CCTCATCATT TTTCTTTGCTG CTGAGCTCCC TCCCCAGAGG TTACCTCTGT  
32001 TCATGGTTTT TGTCATCCGT CTAGTCCCC TGTTACGCGT TTACAGGAAT  
32051 ATGTTTTGCA ACAGTGTTT CATCTAAATA GAATTATACA AAATAGCGAT  
32101 TTCTGATTTC TCTTGCAAT TGCACATTCT TCTTATACTT CCTCCCTACC  
32151 TTTATCTGAC ACAGAAATGC TGTATGTCCA GAACTTCTAT CAGAGGCACC  
32201 TATGGAAGTC TAAGGGAAGA CCACATCGCT TTTAAAAACC CTAAATTTT  
32251 GTAGTCACTA GATGAAAATA TTCAGCCAGT GACCCAAAAA ATTGCTACCA  
32301 ATGAGACTCT CCATTTTGCC ATGTAGCCAG AACTTACTTT GATCTATGTG  
32351 CCTGGGGTAG TGACCAAGTA GGTGGGTAGG AGTAATCTCA GGGAAACTTG  
32401 AGGCCCCAGC CTCATGGCTA GGGTCATAAT TTGAACCCAG GTCTGTCTGA  
32451 CATCAGAATC CATGATGTTA ACCCCAATTC TAAGGGGTTC AACTACCCCT  
32501 TCTAAATGGA ATCCTGCTAT ATTAAGCACT ATTTATTCAT TTTATATAAA  
32551 CTAGAAACAT TTTATGTAGT AAGTAGTTGA GAGTGTTTTG GTTTTGCAGT  
32601 TTGATCACTA GTTTTAGAAA CCAGTTTTTA AACACTTTGT GGCCAATTCC  
32651 ATTACTATAT TAAATTCAG ATTTATTTGG TTTTCCCTTA ACTATTGGGA  
32701 TTAAATCCTG GTTGTAAATC ATAGTTTGAG GGCGAGGGTG GGCAGTCTAC  
32751 ATTTGGCTGA GCCCTGTTT TGTGAATAAA TGTTATCAGA ACACAGCCAC  
32801 ACCCATTTGC TTCTATGTCT TCTGTGGCTG CTTTGTCAAT GTGACGGCCG  
32851 AGTTGAGGAG CTGCAACAGG CGATGACTTG TAAAGCTGAA AATATTTTTT  
32901 GGCCCTTGAA TAAGAGGTTG GCTGACTTCT GACTTAGGGC ATCAGTTGTT  
32951 CTGTTATCCC AGTAAACTC AAGGCATTAG GGGAGAAATG TTAATATTAA  
33001 TACTTAAGTT GATTTGATT AGGGAAATCT TTGAAGATT CTAAGTCTTA  
33051 AGCAGTAGAA CCTGTTAATG GTTTTAGTTT CAGCAGTAAG GACATTTTAC  
33101 AAGTAAAGTT TTAATGAAA ACATTTTGTGA TGAAGCCACA AGTCGTCTGG  
33151 CCTCTTGCTG GTGTCCAGAT ATTAACACTG ATCCTATTTC TCCTTGCTGA  
33201 CCAAGTCTGT CCTTTGTAGT AAGAAAGGAA GAAACGTTGA CTCTGTCCGA  
33251 TCTCTGGACT TAGTGTGTA GCGAGCATGC ACCTGGAAGG GACTTGCCAG  
33301 AGGACCTCCT CATGCTTCTC CAGTGCTTAG TGGGGGCTTG GAGTGCAGCC  
33351 CCAGGTCCTC ACGAGCAGTT GGCCACACTG CAGGGCCCTC ACCCACTCT  
33401 GGAGCAGCCT CTGCTTCAA CCAGCCTGGA TGCTTGTGAG CTGGGGAGAA  
33451 GATCAACCTG CTATTTTGGG ATAGAAATAA ATGCTCAGCC AAACGGCCAG  
33501 AAACCCCAT TCCCCTCTCT GCCAAAGTGA ATTCCTTGGC AGGGAGAAGC  
33551 TTGTTCTGTT CTCTGCACAC TTCCTGTGCC CTCCTGTGGT TAAGTCAGAG  
33601 AATCATCCGG CTCTTTGAGC CCCAGGTGCC TAGCTGCTCA AGGATGGTCC  
33651 CCAGCCAGCA GCTGCCAGGA ATCACCTGGG AGCCCATTA GACATCCAGC  
33701 CCCCACCAA ACCTATCGAA TCAGAATCTG CCTTTTTTTC CCAAATGATG  
33751 TTTTTGCTTT AATGGAAAGT TAGATGTTCA TAGACAAGAG TTTTAAATGA  
33801 TGATCAAGCT GATTCCATAT TCGCAGTTGT AAGTAGAACT GCTGAGACGT  
33851 GGAAGTACCA CATGGACTCA CAGAGGAGCT GCTGTATGTA GCACAGCATT  
33901 GCACAAGAGC TTATTTCACT CTAGTAAACA TTTATAGGAG CCTGTGTCAT  
33951 TTAATCATCA AGCCTCGCAC TGTGGCTCAC ACCTGTAATC CAAAACCTTT  
34001 GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TAAGGAGTTC GAGACCAGCC  
34051 TGGCCAATAT GGCAAAACCC TGTCTCTACT AAAAATACAA CATTTAGCCA

FIGURE 3K

34101 GGTGTGGTGG TGCACACTTG TCATCCCAGC TATTCCGGAG CCTGAGACAT  
34151 GAGCATCGCT TGAAGTCGGG AGGTGGAGGT TGTAGTGAGC TGAGATGGCA  
34201 CCACTGCACT CCAGCCTGGG CAACAGGGTG AAGGCCCTTT CTCAAACTCC  
34251 TCAAGTATTT GGCTTCAACT TTATGCCGGG CATGTAGATG AAAAGTCGGC  
34301 TATGACCTGT CCTTGACAAG CAGATGTAAC TCCTTGATTG AGGCTAGTAG  
34351 GTTTTTAAGA CCTGAATAAT TGAGTTTGCA GAAACCTACT GTGTGCCTTC  
34401 AGGTAAATGG AGAGTGGGGT TTGGTCTAGC AACGAAGCAT CTAGAAGGTC  
34451 TCCTTTGGCCT TACCGGCTCT GTTTTAGGTA AGTCCACGTC TGAGTACCAG  
34501 TGACTGCAGC TCTTCCAGTT GTGCTGTCAT GTTTATATGT TAGAAATGAT  
34551 CATCAAAGGA CTCAAAAGTT TTGCCACTAA TTGTATTACC GGGGACTGTC  
34601 ACAACCAAGA TTTCTCTTAA TTTATTCACT TTACTTATCT CCTGGAAGGG  
34651 CATATTGAAG TGCTCTTGA GTTCTCTAAA AGGGTTTTTG TTGGTTGTGT  
34701 ATATTCACCT GGGTGCCAGC GATTGATTCC AAATAAGTAA ATCTTTTTC  
34751 CCAAAGGAT GTAAGATGGC TTATGGTTAT AAGTACAACA GGCTAACAAA  
34801 GTACAAGTAG ATGAGAAAGT AAAATGAAGA AATAAAGTCA TAGGAGCCAC  
34851 AGAATTAAAC CAGGAATGAA TAAGTGTGTA GTTTGGTGCT GATGTTATCA  
34901 TCCTTTATTT GTACATTGCT TGTACAGTTG CTCTGAGAAG GTAAGTCTTA  
34951 AATTTTCAAA AGTGAAATGT CACCGAGCAT GGTGGCTGAT GCCTCTAATC  
35001 TCAGCACTTT GGGAGGCTGA GGCAGGCGGA TCACCTGAGG TCAGGAGTTC  
35051 GAAACCAGCC TGACTTATGT GATGAAACCC TGTCTCTACT AAAAAAAAAA  
35101 AAAAAAAAAA AAAAAAAAAA AAAAATCCAA AAGTTAGTTG GGCATGGTGG  
35151 CAGGTGCCTG TAATCCAGC TACTTGGGAG GCTGAGGCAG GAGAATCGCA  
35201 TGAACCTGGG AAGTGGAGGC TGCAGTGAGC CAAGATTGCA CCACTGCACT  
35251 CTAGCCTGGG TGACAGAGCG AGACACCATC TTAACCAAAA AAAAAAATCT  
35301 ACAATATACC AAAACCATTA CTTACCTGAG AAATATTCT CAGGGTCATT  
35351 GTAGTGAATG CCTATTTTAT GGCTTTTGAT GGCATCAGGG CACTCAGGTC  
35401 ATTTACAAGA GTAGTGTGTG AGACCTGTG TGTCAC TGCC ACTCATCTTG  
35451 GCCTTCGGCC ACTGCTGTAG CAACCAAGTT CCAAGTAGGG CTGGACCTTG  
35501 CCTTCTGCTC CAGAGACCTC TCGCTTCCTC CCCTTGGGCT TCTGACGAGC  
35551 TGCAGGAAGT GCCTGGCAGC TGGGTCCCA CAACCCAGAG GAGGTGAGGG  
35601 CCACCTCTCT GCTCCTCAGG GCCACCTTC ATAAGGCTCC TTGAAGGTCC  
35651 CTCAAGATCA AGCCAACTCA ACACATCCTT GATAGGCCTT CCTGCCTTCT  
35701 GTTTCACCTC TCCACTCGTT TCCAAATAAA TGGCTGCATG CAAGCTTTTG  
35751 CCTCAGGTTT TGCTTTTAGG AGGAAGGCTA AGACAAGCAG TAAAGCAACA  
35801 TGGGCAGGCA GAAGGATGAC TTCTAATAGA ATTATCTCAT CACTATATAT  
35851 TTTACTTTAT GGATGCTTGT ATTGAAAAGT CTTGGCTGGG TGGAGTGGCT  
35901 CACGCCTGTA ATCCCAGCCC TTTGGGAGGC CGAGGTGGGT GGATCACTTG  
35951 AGGTCTGGAG TTTGAGACCA GCCTGACCAA CACTGGTAAA ACCTTGCTCTC  
36001 TATTAAAAAT GCAAAAAATTA GCCAGGGATG CACGCTTGCT GTGTGCCAGC  
36051 ACAGGGCTAG GCTGGAGATA AAAAGGTGAG TAAGTAGGTG CGGTGTAGTC  
36101 AGGGTGAAAA CTACAGATGG TCCATTTCCTA CGTAAGTGGA AAGGTAAAGG  
36151 TATGTACAAT AGGTGGCTC CTGGCTGAAC CTGGAGCTGC AGACAGGTTT  
36201 TCTAGAAGGC ATAATCCTGA AGTTGAGACT TGGGGGCTA GGTAGGAGCC  
36251 AGTTGAAGGG ACGTGGGAGG CGCATTCAG AGAGAAGGAG TGGTATGAGA  
36301 CTGGAACAGA GGTGTGCAGC AGCATCGCAT GGGCGAAACA ACAGTAGACA  
36351 GTTGTCTCTT TGTTTTTGTT TGTTTTTTGA GACAGGGTCT TGTTCTGTCA  
36401 TCCAGGCTGG AGTGCAGTGG CATGATCTCG GATCACTGCA ACCTCCACCT  
36451 CCCAGGCTCA AGTATCTTC CCACCCAGT CCCCAGTAG CTGGGGGACC  
36501 ACAGGTGCAT GCCACGATGC CCGGCTAATT TTTGTACATT TTGTAGAAAC  
36551 AGGGTTTTTAC TGTGTTGTCC AGGCTGGTCT TAAACGCCTG AGCTTAAGCA  
36601 GTCTACATGC CTCAGCCTCC TGAAGTGCTG GGATTCCAAA CATGAGCCAC  
36651 TGTGCCTGGC CCGGCAACTG TTAGTAGACT ATAGAGAGGG AGGTGGGCAA  
36701 GGGCTGGTGA CACTAGACAG GTGCAGTAGG TCTGGACCAT GGGTGGCCTT  
36751 GCGCTACACA TTACAGAGCT CAGGCTTTTT TTCTCCAGGT GAGAGGGCTG  
36801 GTGCCACTGA GGCATCAAGC AGAGGTTTGA GATCTCCTTG GTGACAGTGT  
36851 AGAGCAGACA GGTAGATTG GGAATTTAAG CTTAGACTCA CGTTGGAGAC  
36901 TGAGATAGCT CATCTGAGAG GCACTCAGGG CCTAATCTCA GGCAGTAATT  
36951 TTAGGGATGT AGGGGAAGAG ATGGATTCTG CACATACTTG GGAGGCTTGT  
37001 GGAGGAGTGG GGAGGGAGGC ACAGGGAGGA CTCCAGGGTG GTTCATACGG  
37051 CTCCCTGCTT CTGTTCTCTG CCCCCTTTGT CAAGCTGTGG TCTGTACTGC  
37101 GTGTTCCATC TTGTTTCTAA GCTGCTTTTG CCCAGTCTTT CCAGCATTTT  
37151 CCTTTCGTCA TGTTAGTCTG TGCCTGTCTA CGTGAACAT GGTGACGTTT

FIGURE 3L

Docket No. CL001201DIV  
Application Serial No. 10/644,021  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

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37201 ATTGGGCCTG GCACTGTGAG GTGCTGGGGA TGTGAAGATC ATTGTGGCTC
37251 AGCCGCTGCT CTCGAGGGCC TCTGGGTGCA GTATGCACAC CTGTGCCTCC
37301 TGTTTGCTCA GGAAGACAGG CTTTGAGATG AGCTGGGGCT GACATCCCCA
37351 CCTTATCATT GGGATGGCTT TGGGTAAGTT ATGTTTCATGT TCTCTGAGCC
37401 TCCCTTTCTT CATTGGTAAA ATGGGTATAA AATACCTGCC AGTGGAGGGT
37451 TGTTGTAAAGT AGCCATGGAA AATGTAAAGC ACATAGCACT TACCATTTTT
37501 TCCTGTGTCT TTAACAGATT TATCATAGAA TCCCCGACTC AGACCCATCT
37551 TCTAGCAAAA CAAGGCAGAT CATCTCCACC ATCCGGACGC AGAATCTTCC
37601 CCACTGTGAT CTGATTTCCT GAAGCCACTA CTCCCCCATC TACCTGTCGT
37651 TTGTCATGCT TTTGGCTGCC CTGAGCTGGC AGTACCTGAC CACTCTCTCC
37701 CAGGTAACAG AAGACTATGT TCAGACTGGA GAACACTGAT CCCAAATTG
37751 TCCATAGCTG AAGTCCACCA TAAAGTGGAT TTACTTTTTT TCTTTAAGGA
37801 TGGATGTTGT GTTCTCTTTA TTTTTTCTCT ACTACTTTAA TCCCTAAAAG
37851 AACGCTGTGT GGCTGGGACC TTTAGGAAAG TGAAATGCAG GTGAGAAGAA
37901 CCTAAACATG AAAGGAAAGG GTGCCTCATC CCAGCAACCT GTCCTTGTGG
37951 GTGATGATCA CTGTGCTGCT TGTGGCTCAT GGCAGAGCAT TCAGTGCCAC
38001 GGTTTAGGTG AAGTCGCTGC ATATGTGACT GTCATGAGAT CCTACTTAGT
38051 ATGATCCTGG CTAGAATGAT AATTAAAAGT ATTTAATTG AAGCACCATT
38101 TGAATGTTCT TACTAGTAGA AAATGATGTG AATTTTCTTT CTGTTGCGCT
38151 CCTATTTTTC TCATCATTTT GTTTTCTTTA ATTGGGTGTA ATGGAGTAGA
38201 TAGAAATATT TATGGTTTAG GTAACAGTTA GATGTTTCCT AAGAATGCAA
38251 ACTGCCTTTT CCACACAAAG GCTGGGAATA AAATTCTGGG TATTCTCGTA
38301 TTCTCATTTA AAGGAGTTTA GCTTTCAGAG AGAAACAGCA GGATTGCTTT
38351 TGACCTTTTA GAAGATTGGT CTCCAGTAAA GGTGGACATT TTTGAGATTT
38401 TTATAATAAA GAATTTAATT GCTCTGCATT TGTCAAGTAC AGTTCGCTTG
38451 AAAGCCTGCC TGACTGTGGA AAAGATGGAG CTCAAGAATG GAGTTGATGG
38501 CCCAGCGTGG TGGCTCATGC CTGTAATCCC AGCACTTTGG GAGGCTGAGG
38551 CGGTCGGATC ACGACATTAG GGGATCGAGA CCATCCTGGC TAACACGGTG
38601 AAACCCCGCT CTCTACTAAA AAAAAAAAAA ATTAGCCAGG CGTGGTGGCG
38651 GGTGCCTGTA GTTCCAGCTA CTCGGGAGGC TGAGGCAGGA GAATGGCTTA
38701 AACCCGGGAG GCGGAGCTTG CAGTGAGCTC AGATCGCGCC ACTGCACTAC
38751 CAGTCTGGGC AACAGAGCGA GACTCCATCT CAAAAAAGG AAAAAATTGT
38801 AAAAAAAAAA AAAAAAAAAA NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN (SEQ ID NO:3)
```

FEATURES:  
Start: 2058

FIGURE 3M

Exon: 2058-2156  
Intron: 2157-7996  
Exon: 7997-8094  
Intron: 8095-8869  
Exon: 8870-9053  
Intron: 9054-25147  
Exon: 25148-25339  
Intron: 25340-29365  
Exon: 29366-29542  
Intron: 29543-30639  
Exon: 30640-30792  
Intron: 30793-37517  
Exon: 37518-37736  
Stop: 37737

**CHROMOSOME MAP POSITION:**

Chromosome # 8

**ALLELIC VARIANTS (SNPs):**

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
825	G	A	Beyond ORF (5')			
2632	C	T	Intron			
4430	C	T	Intron			
4791	C	T	Intron			
4886	G	C	Intron			
4887	A	T	Intron			
4889	T	A	Intron			
5110	G	T	Intron			
6911	G	A	Intron			
7212	A	G	Intron			
7355	C	T	Intron			
7398	T	C	Intron			
7653	T	C	Intron			
8310	A	G	Intron			
8145	C	T	Intron			
8031	G	A	Exon	45	R	K
8462	G	C	Intron			
8873	C	T	Exon	67	N	N
9190	C	T	Intron			
9311	T	-	Intron			
9847	T	C	Intron			
10460	C	T	Intron			
20204	G	A	Intron			
20362	C	A	Intron			
21166	G	A	Intron			
21477	G	A	Intron			
22230	C	T	Intron			
22941	A	G	Intron			
23963	C	T	Intron			
25686	A	C	Intron			
26018	A	G	Intron			
26078	G	A	Intron			
26625	C	G	Intron			
27151	C	T	Intron			
28032	G	A	Intron			
28772	G	A	Intron			
29572	C	T	Intron			
29761	C	T	Intron			
30732	G	C	Exon	281	L	L

**FIGURE 3N**

30841	G	T	Intron
31376	G	A	Intron
32032	A	G	Intron
32525	A	G	Intron
34179	G	T	Intron
34249	T	C	Intron
34451	T	C	Intron
34532	T	C	Intron
36541	T	C	Intron
36607	A	G	Intron
36681	A	G	Intron
37493	C	T	Intron
37966	C	A	Beyond ORF (3')
37973	T	C	Beyond ORF (3')
38113	C	A	Beyond ORF (3')
38298	G	C	Beyond ORF (3')

Context:

DNA

Position

825 CCAGTGAACGTACCTGACAGGTTTCCTGTTTGTGTTTGTAGATGAAGTCTCGCTCTTGTTCC  
CCCAGGCTGGAGTGCAATAGCGCGATCTCAGCTCACTGCAACCTCTGCCTCCTGTGTTC  
AGCGATTCTCCTGCCTCAGCCTCCCAGGTAGCTGGGATTATAGGCGCCTGCCACCATGCC  
TGGCTAATTTTTGTATTTTAGTAGAGACGCAGTTTCAGCATGTTGGCCAGGCTGGTCTT  
GAACTCCAGACCTCAGGTGATCCGCCCGCTTGGCTCCCAAAGTCTGGGATTACAGGC  
[G, A]  
TGAGCCACCGCGCTCGGCTAGACCTGACAGGTTTTAAAGGATTACTGGTTGCTGTGTTA  
AAACAGACTGCAGGATGGCTTAGGTAGCCAGTAGGTTTTTTTTTTTTTTGGAGACGTAGT  
CTTGCTCTGTTGGCTGGCTGGAGTGACGCGGTGTCATCTTGGCTCACTGCAAACTCCGC  
TTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCGGAGTAGTTGGGACTACAGGCGCC  
CACCACCACACTCGGCTTTTTGTATTTTAGTAGAGACGGTTTCACCATGTTGGCCAG

2632 GCCGTCCTGGCTGACCTGTCCCTGCCCCGCAAGCCGCCCTGGGCATGAGCGACTTTTGC  
GTGGTTCCCGGTGGTTGCGCTCCCGTTTCGTCCCTCCGTGAGCATCGGCGCTTACCGG  
TATTTTAACCCGAGGTTACACATCTGAGGCAATGTGGGTGGTTACGCGGAGAGGACG  
AGTGAGTTTTTTGGTAAGCGGAATGAACTATGCAGATAACATCACATGAAGGCCGTTTCT  
GGAATGAAGTCTGACTCCTCCAGTTTCACCACCTCTCCGGAGCTCTCCCGCCTTGCTG  
[C, T]  
CTTCCATCGCTTCATCCTCGGTGCTTCTGAGTTTTAAATCGCCTATCTACGCTTCCAA  
GTTCCAATGAGTTATCTAACGTCTATGGATTAGCTAGGTGGTTGGTGAAGGTCAGAACT  
TGGTTTTACTTAGATTTTTATCTGCCTCATGCCGTACTATTGTTAATGAATGCATAG  
GAGGTGTTTTTATTTCCAACAAGAAAATTATTTCGTACGCGATTATTGAATGAATAGACAAA  
TTCAGCCAAGTTCTTCTGGTCTGGACCAGCCTGGCTGATTTCTGTAACTTTTTTGGGCCA

4430 GGCCTTTTTTTTTTTTTTTTTTGTAGGGGGGGTCTCACTCCATCGTCCAGGCTAGAATGCT  
GTGGCCTGAACATGACTCACTCCAGTTTGACTTCCTTGGCTGAAGCCATCCTCCCACCT  
CGGCTTCTGATCCCGAGTAGCTGGGACTCCAGGCACGTGTACCAATGCATGGCTAATT  
TTTAAATTTTTTTGTAGACACAATGTCTCGCTGCATTGCCAGGCTGGTCTTGAACCTCT  
GAGCTCAAGCGATTTTCCACCTCAGCCTTCAAAGTGCTGGGATTACAGGTGTGAGCCAC  
[C, T]  
GCACCCAACCAAGTTTCTCTCTGCAAACTAGGGAAAAAATTTACGCTTAGCAGATATTGAG  
GGCTGATTATTTCTATCACAGAAGCATTTGGCTATAGAATTTACAGGTTTAGTAAACTTG  
ATTTACACTGAATTTTGGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT  
TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAGAGCAGGCTGTTAGTAATCAGGCA  
GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT

4791 GGCTGATTATTTCTATCACAGAAGCATTTGGCTATAGAATTTACAGGTTTAGTAAACTTG  
ATTTACACTGAATTTTGGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT  
TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAGAGCAGGCTGTTAGTAATCAGGCA  
GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT  
AAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAACCTTGGTAACTTAACCTCTGAAC

FIGURE 30

[C, T]  
ACAGTTACTTCATCTGTAAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAAC  
TCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCAGTTGGC  
AGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTT  
GCTAAAGAAATAATTATGAGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTAT  
TGCTATTTTTCTAAACACTAAAAATGCTAAATTCTGCCCCAGGTCTTGCCACAGATGTT

4886 CTACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAA  
AGAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTT  
AGACTAATATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAAC  
AACCTTGGTAACCTTAACCTCTGAACCACAGTTACTTCATCTGTAAATAGGGATGTATGT  
ATGGTAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTT  
[G, C]  
AGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCAT  
CCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACT  
GACTAGGGTTGTATATGCATTTTATGCTTATTTCTAAACACTAAAAATGCTAAATTC  
TGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT  
TGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTG

4887 TACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAA  
GAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTA  
GACTAATATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACA  
ACCTTGGTAACCTTAACCTCTGAACCACAGTTACTTCATCTGTAAATAGGGATGTATGTA  
TGTAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTG  
[A, T]  
GTGTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATC  
CCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTG  
ACTAGGGTTGTATATGCATTTTATGCTTATTTCTAAACACTAAAAATGCTAAATTC  
GCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT  
GATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGA

4889 CGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGA  
GCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGA  
CTAATATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAAC  
CTTGGTAACCTTAACCTCTGAACCACAGTTACTTCATCTGTAAATAGGGATGTATGTATG  
GTAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAG  
[T, A]  
GTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATCCC  
ACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTGAC  
TAGGGTTGTATATGCATTTTATGCTTATTTCTAAACACTAAAAATGCTAAATTCCTGC  
CCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGTTGA  
TTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGATA

5110 AAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAACCTCCCAACTCTAAGATGGT  
CTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAA  
GTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATG  
AGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTATGCTTATTTCTAAACA  
CTAAAAATGCTAAATCTGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCT  
[G, T]  
TGAGACCTTAAAGGGTTGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCA  
TGGAGTTAAGTGCTTGATAAATGGTGGTTATCAATCTGATTATGTAAATTTATGTAAATT  
CAGTTCTCAAGTTTGTGGTTTTTTTCCCCTCCTGGAGAAATCTATTCTATTTTAAAGTGA  
GGAAGGCTCCGTGGAGGGCTGGTAGCTGGTAGCTGTTCACTTGTGGAACCTTTCAGCCTGA  
GGCTGGAGCCCCCTTCTGGGAGTCTGGTCTTGTGCTTCTTGACCACCCACACCCCTT

6911 CCACCTTGGCCTTCCGAAGTGCAGGGATTATAGGCGTGCGCCACTGCACCCGGCCCTGTT  
GGATAAATGATTCCAGTCTCTCCCAAAAAGAACTGTTGTAAGACTGTGGGGTGAAGGGAG  
GGAAGGGACAAATAGGAACCCGCCGTATTTTCCACTCCCTGTGGGCCTAAACTGCTCTA  
AAAAATAGTCCATGAAAAAATACATAGTACAAACAGCAACTCTTCTGATATGCTTGCA  
TTAAATCAGGCTTTTTCTCCCTTTTGGAAAAACACAGTCTTGTGCTTTAGGGAAGA  
[G, A]  
TAAAGGTCAGTGCGCTGCATTGCATTAATTTTGAAGGAAAGATGAGAAGACATCTTGAA

FIGURE 3P

AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG  
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG  
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCCAATACAAAGAAAAGTAGGAATTGA  
TGGCGGGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGC

7212 TAAAGGTCAGTGCCTGTCATTGCATTAATTTCTGAAGGAAAGATGAGAAGACATCTTGAA  
AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG  
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG  
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCCAATACAAAGAAAAGTAGGAATTGA  
TGGCGGGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGC  
[A, G]  
TTCTTGCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGG  
AACCTAATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAA  
TTTAGCAGGATTCTTGGTAAACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTC  
CAGGCTTTATTGGGAAGAGGATTTAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACT  
CTGTCACTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGT

7355 CAAAACAGATTTTATTAGAAAACTACTGCAGTAAGAGGAGAGAGACCTCGGTACAGAA  
CTGCTCCACTGCCAATACAAAGAAAAGTAGGAATTGATGGCGGGGAGCCGGATGTCAGT  
GGATGGAAAATTATTACGAGGAAACACAGGGGTGTGCATTCTTGCTGAAGGCAGGCCAGA  
GTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCTAATCGGCTGTCTAGGGT  
GATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAGCAGGATTCTTGGTAAAA  
[C, T]  
TGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGGATT  
TCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGCGAG  
CCGCTCGGAAGTGCCTGGGTTCTCTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCAACA  
GCGGGAGGAGGCGCCGGTGCGGAGCGGGAGGCCGGGGGCGGGGCTGCGGGGTGCGGGGC  
GGCCCCGTGTGGGTGCGCCCAGCGCGTATTAGTAGAGGGCGAGCCCGTCCCGCTCT

7398 GAGACCTCGGTACAGAACTGCTCCACTGCCAATACAAAGAAAAGTAGGAATTGATGGCGG  
GGGAGCCGGATGTCAGTGGATGGAAAATTATTACGAGGAAACACAGGGGTGTGCATTCTT  
GCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCT  
AATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAG  
CAGGATTCTTGGTAAACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGC  
[T, C]  
TTATTGGGAAGAGGATTTAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCA  
CTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTT  
TGGTGAGAAGGGCAACAGCGGAGGAGCGCCGGTGCGGAGCGGGAGGCCGGGGCGGGG  
CTGCGGGGCTGCGGGGCGGGCCCCGTGTGGGTGCGGCCAGCGCGTATTAGTAGAGGGC  
GAGCCCGTCCCGCTCTCGTGGGCGCTTCCAGATCTGCTTGAAGTCTATGGAGGAAAAA

7653 AACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGG  
ATTTAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGC  
GAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCA  
ACAGCGGGAGGAGGCGCCGGTGCGGAGCGGGAGGCCGGGGGCGGGGCTGCGGGGCTGCGG  
GGCGGCCCCGTGTGGGTGCGGCCAGCGCGTATTAGTAGAGGGCGAGCCCGTCCCGCC  
[T, C]  
CTCGTGGGCGCTTCCCAGATCTGCTTGAGTCTATGGAGGAAAACTCCGCGGGTCCGC  
GATTTCCATGGCCGCGAGCCGCTGCGGCACCAAGGCCATGGCCCTCTTCAAGCGCACCTT  
GGTGCTGAGTCCCGCGCGCGGCCAGGGGCCCGGCGCAGGACCCGCCCCGCGGGGCTG  
CTGCTTGCCCTCTGCGGCTGCGCCCTGCAAGGACTGGCTCGGGGAGAGGGCGGCAGGCT  
GTGGAGCCGCTGCCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGT

8310 CAGCCTGAAAACCTTGCTACAAGTATCTCAATCAGACCAGTCGAGTTTCGCAGCTGTTAT  
CCAGGCGCTGGATGGGGAATGCGGTGAGTGATGGAGGCAGCGCTCTGGCTTGAGGAA  
AGCTTGTCGGGACTTTTGAAGTGTGTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTG  
CAGCCTCGTTGCTGTGGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAA  
GCCCTTCCAGGCTTTTGCCATCTAGTAGAGTCCCTGCGGGCCAGCCTTTAGAGAAAG  
[A, G]  
GGGGGAGGGGGTGATGTTTATTAACCTTTTTTTAGTCTTGGCAGCTGAACCTGCCTGTGA  
GCAGGTCGTGATTTCTCGGCTTCCCTTATCCAACCTTGCATTTCTATTTCTAGCATATT  
GGGTTGATTCTTTGAAGCTGCCTCTGTGCACATTACACCCATGAACCTTAGACCAGTTGC

FIGURE 3Q



CTTTATGTATGATCGTATTTATACTGAGAAGTTACTGTGTTTTTGGACTTTCTTTTCTAT  
TTGCTACATATTAGTTCGGTCTAAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTG

8145 CAGCCTGAAAACCTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTAT  
CCAGGCGCTGGATGGGAAATGCGGTGAGTGATGGAGGCAGCGCCTCTGGCTTGAGGAA  
AGCTTGTCCGGGAC  
[C, T]  
TTTGAGTGTGTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGT  
GGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCCAGGCTCT  
TTGCCATCTAGTAG

8031 CAGCCTGAAAACCTTGCTACA  
[G, A]  
GTATCTCAATCAGACCAGTC

8462 GCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGTGGCTTATCCAGAACAT  
AGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCCAGGCTCTTTGCCATCTAGTAGAG  
TCCCTGCGGGCCAGCCTTTCAGAGAAGGGGGGGAGGGGGTGATGTTTATTAACCTTTT  
TTAGTCTTGGCAGCTGAACCTGCCTGTGAGCAGGTCTGTATTTCTCGGCTTCCCTTATC  
CAACTTTGCATTTCTATTTCTAGCATATTGGGTTGATTCTTTTGAAGCTGCCTCTGTGCA  
[G, C]  
ATTACACCCATGAACCTTAGACCAGTTGCCTTTATGTATGATCGTATTTATACTGAGAAGT  
TACTGTGTTTTTTGACTTTCTTTTCTATTTGCTACATATTAGTTCGGTCTAAACGTTTGG  
TCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGGAGTAGTGGTG  
ACATTCAACTAGTAGGCTTTTTAATAAACTACAGAAGTTCATTACTCTCATGTAAGGAAG  
GAAACTAATGTAACTTTCGTTAAGTATGAAAAGCGTTGGATATCCTTATAGTTCTTTAG

8873 AAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGG  
AGTAGTGGTGACATTCAACTAGTAGGCTTTTTAATAAACTACAGAAGTTCATTACTCTCA  
TGTAAGGAAGGAAAATAATGTAACCTTCGTTAAGTATGAAAAGCGTTGGATATCCTTAT  
AGTTCTTTAGAGTTAAGGGTGAGATGGGTTTAGAAAGTGCCAGGCACAAGTTATTTTAA  
AATAAAAAATCTTTGGCTGTTTGTTCGAATATATTAATAGTTTTCCCTTTTTTACAGCAA  
[C, T]  
GCAGTGTGCATATTTTATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACC  
ATCAGTGTGGAAGAAGGTCCCGCTGTACACAACCTTCACTCTTTCCTTTACCAACCA  
GACTGCGGTTTCATGGAGAGCAAGGAGGATCGCCAGGTGCTGGAGGACTTCCCAACG  
GTGAGTGGGGTTACGCATCTTGTCTACGGAAGTGTGTGTTTATAATTGCTAACGTGGTTG  
TCCGGTAGCCTCCATACATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATG

9190 ATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACCATCAGTGTGGAAGA  
AGGTCCCGCTGTACACAACCTTCACTCTTTCCTTTACCAACCAGACTGGCGGTTTCATGG  
AGAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGC  
ATCTTGTCTACGGACTGTTGTGTTTATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATA  
CATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTTAAAAACTC  
[C, T]  
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA  
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG  
TAATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACGTAGGTAATGCT  
CTTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTTCCTGTG  
GGAAGACGCAGTCAAATTTTAGTGTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTG

9311 GAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGCA  
TCTTGTCTACGGACTGTTGTGTTTATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATAC  
ATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTTAAAACTCC  
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA  
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG  
[T, -]  
AATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACGTAGGTAATGCTC  
TTAGAAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTTCCTGTGG  
GAAGACGCAGTCAAATTTTAGTGTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTGC  
CGACTGTATGATGCAGCCTACCTGTAACACTGCTGGCCTCTTGACTACCCGGAGCCTGGT  
AGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGCGGTGTCTGTGGCA

FIGURE 3R

9847 CTGGTAGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGCGGTGTCTGT  
TGGCAGCTAGGGCGAGCCTCTGCCACTTCACCTGTGATCCTGGGCAAGTTCCTTATCTGC  
TTTGTGTCTCCGTCTCCTCGTTTGTAAAGTTAGAGCTGAGAGGATTAATTTGCGACATAT  
AAAGTACTTAGTGCCTGGTACAGGGTAAGTATTCTGTAAGTATTAGCTATTTGGTCTATT  
TTGTTGGAGTAAAGTGGGTTATAGTTAAAATCCTAAGATTTTTTAAAGTCCCTCAAGTTCA  
[T, C]  
GTGGACATCTGCCTAGGTCCTACTATCCTAGAATTTCGCATGTCTTATCACACAAATAACT  
GATTCTTCCATATCTTATAAATAAAGGTTTGATTTAGCAAAGTCACATGTTGTGTAATAG  
CTCGAAGAAGCCCTTTTGTCCACAGTTGCCAGAGCTTTTGGAGAACAGTCCTTATGTTA  
TTGAAACAAACCTAATCTGTAGCTGAGTTGGGAGGGAGCTAAGTGGACAGAGAGTCTCC  
ACCCAAACAAAAGAACTTTGATTCTTGGGCATAATGGGAGCAATATTTAAAAAATAA

10460 AGGAATGTTTGGGGAAGACTCTTGCGGTGCAAAGGCTGTTTCAGATTGCTGAGATCAGAC  
CTTAAGTACCAAAGCCCAAATATAGTACAACATAATACAAATGAGAAGAAAATAGCTGAA  
GAATAATTCGAGTTTATACAGTACAATTCAAGAGAAGAAAGAAAATTTATGACGACTAGC  
TGGGTGAGAATTAGAACTGTAACCTTGGGAAGGTCCTGGTGATTGACTCTCACAGGACA  
CCTGATGACCAGAGGATGGGTTTCTTTGATGGGAAATCTGTGGCGATTCAATTGATGGGC  
[C, T]  
TCTGAATTCTGCTGAAGCAGAGGAAGTAGTAATACCCCATTTATAATGGAAGTGCATTCT  
CACTTAAAAACAATAATATTCTAGCTGGACCTAGCCTCTAGAAAACAGCCAAATTAC  
ATTTGACTTGAGTGGATTCAATAATTAATAAATTTCTGGGCGATGGGATAAATGTGTT  
AGGTATTGCTAAGTCAAGGCAGCCCTATCCCCTCAGCAGAAGTGAGGGAATATGAAAGTG  
TGTGAATGCTAACATAATTTTGGGGAATATCGCCGTCAGATTTCCAGATGATATTCCAAC

20204 TCTGCCAGTTGCGAAGACTGGGAAAAGCACAGTATTTGGGCAGAGTATACTGTTCCCTCA  
GGTACAGTCACTCACGCCTTTCTTTGGCTAGGAAAGGGAAATCCCTTGACCCCTTGCACT  
TCCTGGATGAGGTGACGTCCTGCCCTGCTTTGGCTCACCCCTCCATGGGCTGCACCCACTG  
TCCAACCAAGTCCCAATGAGATGAACCAGGTACCTCAGTTGGAATGCAGAAATCACCCAT  
CTTCTGTCATCGATCTTGCTGGGAGCTGTAGACCAGAGCTGTTCTACTGGGCGATCTTGG  
[G, A]  
AGCAACTCTGGGTCTGAGTTTCTGTTTGTGTCCTGATGTATATCCCCAGTGCCTAGAAT  
GATACTTGTTACATAGGAAGTGCTTGATCCATGTTTGACACAAATGAATCTTTCTCATAT  
GAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACCTTACACCCAGCTTTATGTTGAAGCAT  
CTCATTATACATTGGAAAGATGAAATGTGTAGTGAGACTTTGAATCTTCTTTGAATCTA  
GAAACATTAGCATTTTATAGACCATTCTATTTTAATATTTATGAAATTTATGAAATAATAA

20362 CCTCCATGGGCTGCACCCACTGTCCAACCAAGTCCCAATGAGATGAACCAGGTACCTCAGT  
TGGAAATGCAGAAATCACCCATCTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGC  
TGTTCTTACTGGGGCATCTTGAAGCAACTCTGGGTCTGAGTTTCTGTTTGTGTCCTGA  
TGTATATCCCCAGTGCCTAGAATGATACTTGTTACATAGGAAGTGCTTGATCCATGTTTG  
CACAAATGAATCTTCTCATATGAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACCTTA  
[C, A]  
ACCCAGCTTTATGTTGAAGCATCTCATTATACATTGGAAAGATGAAATGTGTAGTGAGAC  
TTTGAATCTTCTTTGAATCTAGAAACATTAGCATTTTATAGACCATTCTATTTTAATATT  
TATGAAATTTATGAAATAATAAGAAACATGAGGCCGGGCTCAGTGGCTTATGCCTGTAAT  
CCCAGCAGTTTGGGAGGCCAGGGCTAGTGGATCATGAGGTGAGGAATTTGAGACCAGCTT  
GGCCAAACATGGTGAAACCCCACTTCTACTAAAAATATAAAAAATTAGCTGGGCGTGGTGGT

21166 TAATTCGCCCATTTGTTTGCCTTGTGATCTTTGGTGCCATGTCTGTACATATTTTCATGATT  
TCTGTGTTTTTACGGTTTCCATTTAGATCTCCCTTGAGTTTAGAAATCTGGCTGAGAAA  
TACCAAACAGTGATTGCCGACATTTGCCGAGAATGGGCATTGGGATGGCAGAGTTTTTG  
GATAAGCATGTGACCTCTGAACAGGAGTGGGACAAGGTTAGTCTCATAAAAACAGTGTCTG  
TGTGTGATGTATTAGACAGAGCTGGCAGTCCTCATAGTGAAGCTCAGAACAAGAAAAGTT  
[G, A]  
TCCAGTATTTTTCAGCCCTCTGGTTTACAATTTCATCTGTTTAGGTTGAATGTCTCATCA  
TAAACAGTTTATTCAGAGTTAATTCCAAACAGCAGCTATGTAGGATATCAGCCAGGCT  
AGGAGTAGGGTACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAG  
ATTAATACTACACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCTATTTTTCATAGGA  
ATGGTGTGTTGTGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTATTTAT

21477 TCAGCCCTCTGGTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCATAAACAGTTT

FIGURE 3S

ATTCCAGAGTTAATTCCAAACCAGCAGCTATGTAGGATATCAGCCAGGCTAGGAGTAGGG  
TACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAGATTAAACCTA  
CACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCATTTTTTCATAGGAATGGTGTGTG  
TGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTATTTATTTTAAAGCCA  
[G, A]  
TCAGATTTAGCAGGCAGAGACATTTAGACATCTAAAGTGTTGATGTATTTACATACCTTT  
AACTGTGCTTAAATTAGGATCTCCGAAAAGATGCTGCTACATGGTCACTACGTTAGTGTA  
GGTCCAAGGTCTTGGGCCTCTTAATTTTTCAAACCTCAAACTTGACAGCAGTTATCTTT  
GGAACTGCTGATTTGTGCTTCCTAAGTTAACAGCATACAATGACTGCTAGAAATCAATTT  
CTGCATTTAAGGTGAAGTTAGCCGGGTACTATGGTTTACCTGTAATCTCAGCACTTTGGG

22230 GGATTGCTTGAGCCCAAGAGTTGAAGGTTGCAGTGAGCCATGATTGTGCCACTGCACTCC  
AACGTGGGTGACAGAGCAAGACACCTACTGAAAGAAAATAAAGTTGAAGTTAAACCTTCT  
GGCCAAGAACCAGCACTGGTTATGATAGTAACTCATTTTCTGTTGTGCAGATTTATTCAG  
GAACTTAATTTTAGGTTGTTGAATAGAAGTTTGTATCAGATAAAATGAATTAAAAAA  
ATTTTTTTGGAGACAGGGTCTTGCTGTTATCCAGGCTGGTGTGTAGTGGTGTGATCACGG  
[C, T]  
TCCCGCAGCCTCAACCTCCTGGGCTCAGGTGATCCTCCACCTCAGCCTACCGAGTAGC  
TGTAACCTACAGTGATGACACCATACAGGCTCATTTTGTACATTTTGTAGAGAGAG  
GGTTTGTCCATGTTGCCAGGCTAGTCTCAAACCTCCTGGCATCAAACAGTCTCCCACTC  
TGGCCTCTCAAATGTTGGGATTACAGGCATGACAGCCAATTATTTCAAGGAGTTATTTT  
TTTTCTTCTACTTTGGGGGAAGATGAATTATATAAGTCTCCATTTTAGGAGTATTTCTAC

22941 AATTCTGTCTACCTAATTTAGCAAGATTTCACTCTTTTCATGTTACTTTTGTCCAGA  
ACAAATTTCAAGTGCTTCTCTTACCTGTGCATTCTCCCCCTGATTAGTCTCTGGCTT  
TGTATTACTTTTCACTGAGAGACGACTTTTTTTTTTTGAGACAGGGTCTCACTCTGTCCACC  
CAGACTGGAATGCAGTGCCACAGACAAGGCAGCCTTGACCTTCTGGGCTCAAGCAATCTT  
CCTTGCCCTCAGCCTCCTGAGTAACTGGGACCACAGGCACGTTGCCACCATGCCTGGCTA  
[A, G]  
TTTATTTTAATTTTTATTATTTTTGAGACAGGGTATTGCTCTGTCACCCAGGCTGGAGTG  
TAGTGGCATGATCAAGGCTCACTGCAGCCTTACCTCCTGTGCTCAAGCAGTCTCTCAC  
CTCAGCCTCCCCATTAGCTGGGACTATAGGTCCACACCACTACACCAGGCTAATTTTTGT  
AATTTTTTGGTAGAGACAGGGTTTCATCGTGTTGCCTAGGCTGGTCTTGAGCTCCTGGGC  
TCAAGCGATTACCTGCCTTAGCCTCCCAGGTGTGAGCCACTACACTCAGCCTTTTAAAA

23963 ATACTACCTAGTTTTGAACTCTTAGCCCTGCCACAGACACGGCAGCCCTTGAACCTTC  
CTGGGTTCAAGCGAGCCTCCTACTTCAAGCCCTGAGTAACTGGGACCACTGGCCTGTGT  
CACTGTGCCTGGCTAATTTTTTTTTTTTCTCACATGGGCAATGTTGGGCAAGTTAAATC  
GACTTCTTTGTGCCTCAGTTTCTCATCTGAAATGGAGATCATACTGCTATGTACCTGAT  
ACAAATGTTGTGAGGATTGAATGTGCAGAGTTCTTTTTTCTGTTGTGTTGTTTGTAGA  
[C, T]  
GGAGTCTCACTCTG

25686 CTGAAAAATCCTTTAACTCTTGTGGTTGCGGGTGACAGAAAAACAAGCCAGGCCTCCCC  
AGGCAGCATAAGGGGATGTGGAATAAGGATAGATTGACATGAGTTTGCTTCAAGGTAGAC  
TGGCTGACTCCCAGGATTCACACCACGTAATCAGTATATTCAAGCCTTGCTGTCCTTGAT  
TTCTTTTCAAGCGTCTTCTCCAAGTGTTGGATATGGTAAACCCACGTGCACTAGCTT  
AACAAAAAGTTCTTAGGAATGGCTTTGTTGCGCCTGGCGCAGTGGCTCATGCCTGTAATC  
[A, C]  
CAACAGTTTGAAGGCCAAGGTGGGCGGATCACCTGAGGCCAGGAGTTGAGACCAGCCT  
GGCCAAATAGTGAAACCCCGTGTCTTAAATAAATAAATAAATAAATAAATAAATAAATAA  
CAAGGGCTTGTAATCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG  
AAGCAGAGATTGCGGTGAGCTCAGATTGTGCCACTGCACTCCAGCCTGGGCGACAGAGTG  
AGACTCCCTCTCAAAAGAAGAGGAAGGGCTTGGTTCTTCTGCTCAGCCCTGAATCAGTTA

26018 ACCTGAGGCCAGGAGTTGAGAGCCAGCCTGGCCAACATAGTGAAACCCCGTGTCTTAA  
AAAATACAAAAATTAGCCGGGCGTGGTGGAAGGGCTTGTAATCCAGCTACCTGGGAGG  
CTGAGGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC  
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAAGAAGAGGAAGGGCTT  
GGTTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGTACACAGCTGAGTTCTCTGGCCTC  
[A, G]  
CCTGGATTACGTCTACACAGTACACACAGAATGGATTTCACCAAGAAAGAAATCTGCC

FIGURE 3T

GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA  
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTTGTT  
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTACCTTTT  
GCTTTCATAAAAGTGTTTCTGCAGCCAAGTACTTTAAAGTTTAAAAAGACGGGTGAG

26078 AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCCAGCTACCTGGGAGG  
CTGAGGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC  
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAGAAGAGGAAGGGCTT  
GGTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGCTGAGTTCTCTGGCCTC  
ACCTGGATTACGTCTACACAGTACACACAGAATGGATTTCCCCCAAAGAAAGAATTCTGC  
[G, A]  
GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA  
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTTGTT  
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTACCTTTT  
GCTTTCATAAAAGTGTTTCTGCAGCCAAGTACTTTAAAGTTTAAAAAGACGGGTGAG  
GCTAAGTGTTGTTCTCATACTTATAATCCCAGTGCTGAGGCCAGGAGTTCAAGACCAGC

26625 TGTGGTGTCTCATACTTATAATCCCAGTGCTGAGGCCAGGAGTTCAAGACCAGCCTGAGC  
AACACAGCAAGATACCATCTCTATAAAAAATTGTTAGAAAATGATTCTGCTGAAAGAGCA  
AAAAATAAAATTAAAGAAAGTAGAAAAATAAACTAAATTTAAAGATTAACTGGGCAT  
GTTGGCATGCACCTGTATTCTTAGGTATTGGGAGGCTAAGGCACAAGGATCCCTTGAGC  
GCAGGAGCTCAAGGTTGGATTGAGTTGTAATCACACCACTGCCTCCAGCCTCGGTGGCA  
[C, G]  
AATGAAACTGTCTCAAGAAAAAAGAGTGACAGAGGGAAACAATATTTGCAATTCATA  
GAGCAGATACAGGGTTCATATTCCTAATATTAATAAACTTCTAAAGTTAAGAAAAAG  
GCCAACTGCCCCACAGAAAATGGGCAAGGAGATAAGAACAAGATTGTTACAGGAAGAG  
ACACACAGATGATTATTAATAATCTGAAAAGATGCTGAGTCTTACTCTAAGAAAAATTC  
ACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGTAATCTCAACTGGG

27151 TCCTAAGAAAAATTACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGT  
AATCTCAACTGGGAGACCAAGGCAGGAAGATCACTGAAGCCAGGGTATCGAGACCAGC  
CTGGACAACGTAGTGAGACCTTATCTCTTAAACAAAAACAAACAAAAACAAAAA  
AACAGTAAAAATTGGCCGGGCACAGTGAATCCTGCCTATAATCCCAGCACTTTGGGAAGC  
CCAGGTGAGTGGATCACTTGAGGTGAGTGTGAGAACAGCCTGGCCAACATGGCAAAA  
[C, T]  
TCCGTCTCTACTAAATTACAAAAATTAGCCAAGTGTGGTGGCATACTGCTGGTAGGGCCA  
GCTACTTGGGAGGCTGATGTGAGACTCCATTTAAAAAATAAATCAAAAATTAGCTGGG  
TATAGTGGCACACCCCTATAGTTCTCGCTCCTTGGGAGGTTGAGGCAGGAGGATTGCCTG  
AGCCCAGGAGTTCAAGGCTGCAGTGAACCATGATCACACCACTGCATTCTAGCAGCCTGG  
GAGACAGAGCAAAACCCCTGTCTCAAAACAAACAAACAACAACAAAAACAAAAACACTT

28032 AGGAGCAGAGCCCTGCTCTTCTCACTTACTTTATCTGTAATAAGCATCATTTCTA  
CCACACGGTGGTGTGAATAAAATGAGATGAATCTTAGCATAGAGTGCTTAGTAAAG  
GTTCTGGACATTTCTAGTAGTTGAATCATGCCAAATGTGGTCTTAGGTGATTGGCTTCT  
TTTGCTAGCATGTTTTCAGGGCTCCTCCATGCTGGGGCATTGCATCACTGCTTTATTCCT  
TTTTATCGCCTAGTATTATCCACTGTGTGGATAGACCACATTTATCCATTATCAGTTG  
[G, A]  
AGGATATTTGGGTTCTTCCCATTTTTTTGGCTATGGTGAATAGTACTGTGTACATTTGC  
ATATAAGGTTTTGTGTAGATGTGTGTTTTCTTTTTCTTGGGTCTATGCTGAGAAGTGGA  
ATTGCTGGTTCATACAGCAGCTCGAACCTTGTGAGGAGCTGCCAGACGCTTTTCCAAGGT  
CGCTCCACCATTTTACATTCCCGTCAGCAGTGTGAGAGTCCAGTTTACCAGCACTTGT  
TGTTATCTCTTTTTAACTGTATGTATATATACTTAACATTTTATTTATAATAAATGTACA

28772 AAAATCATCAAGCCGAATCCCAGTGTAGAAATTAAGGTTTTATTTCACTTTCAAGTTA  
TCAGGATCCAGGGAGGTGTAATACTTAGAGGATAGACTCAGCTCATTTCCAGCTATG  
CCTTTACAGCAGCATTTACCAGAGTAGGAATATAATGTTAGTCATTATTTAGAGGCTG  
GCCATCTTGAGAAGGTTTACTGTTTGTCTGCAGTACAATTATAACTGTTTTTGTATATT  
GGGTTATTTTTTTCAGAAGTAGGCCAGTAGCTCTAACAGGAGCCTCTTAGCCTGAATTC  
[G, A]  
TCCAAGTAGTGAGTGTGCACTAGTTGTCCCTCGGGACATGCTCCCCAATACGTAACCTC  
ACTTCCAGGTTGCACTGGACACTTACTGGTAGTCAGAAATAGCTATTGCATGGAGCTTA  
AAATGAACCTTGATCTTCGTGAAAGATGAGTCTGCAGCTAAGAGACTTTACTGTATATCAT

FIGURE 3U

AGTGTGTTTTTTTTGTTTTGTTTTGTTTTGTTTTGTGACGGAGTCTCACTCTTTCACCC  
AGGCTGGAGTGAATGGCGAGATCTTGACTCACTGCAACCTCCGCCCCCTAGGTTCAAGC

29572 TCATAGTTCTTATGCACAAAGACCCTTTAATATTGTTTGTAATTTCTCCCCTATGCACAC  
GCTGACCTGTTCCCTAATCTTCTTATCTGTCTAGGTTTGGAGCAGGTATGTTAAGAAGTT  
AGGGGATTTTGCTAAGCCGGAGAATATTGACTTGGCCGTGCAGTGCCTGAATGAACCTTAT  
AACCAATGCACTGCACCACATCCCAGATGTCATCACCTACCTTTTCGAGACTCAGAAACCA  
GAGTGTGTTAACTTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATA  
[C, T]  
GGGGCTAAAGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATA  
TGATTCCCTTAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCC  
TTTGCTTCCAGCCACCAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAAC  
CTTCTTTCCGGATTACTATTTTCTACAGCTATCCTAACTAGTTAGGTTCTTTTCCTCA  
CAGTTAAGTCAAGGTCTTTGGCTTAGATTTATGGGAGTGCTGGGTAAAACCTGGGTGAA

29761 ACTGCACCACATCCCAGATGTCATCACCTACCTTTTCGAGACTCAGAAACCAGAGTGTGTT  
TAACCTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATACGGGGCTAA  
AGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATATGATTCTT  
TAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCCCTTGCTTC  
CAGCCACCAAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAACCTTCTTTC  
[C, T]  
GGATTTACTATTTTCTACAGCTATCCTAACTAGTTAGGTTCTTTTCCTCACAGTTAAGT  
CAAGGTCTTTGGCTTAGATTTATGGGAGTGCTGGGTAAAACCTGGGTGAAGCTGTTATC  
ATTAAAAAGTCTTCATTAAGCACCTAATTACTGCTGTCTCTTTTCCTAGACCCGGCATAAA  
AAGAACCTGGTCCGGTAGACCTAGCCTCTCAGTATGCTAGGAACTTACACTTTTTAGTTG  
CCTTTACCAAGTATTGCAGATACTACTGCAAATAAGTGAAGAAAGTAACAGCATTAACT

30732 ATTCTGTGTGTTGTTGAGAAAGGGAGGAGTGGGGAAGGTAAAAATCTTGACATACTTTCT  
TCGTGGGTATTTTCTTGAGCGATTCCATCTTAGTTGATTAGCAGTTAGCAATTGCCCA  
TTCAACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACATCATTTCTTCT  
TTTTTCCCTCTCTTCTGTTGTCTCTAGGTGATGGCCATTGCCACTTTGGCTGCCTGTTA  
TAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAGGGCAAGCAGTGACCTT  
[G, C]  
ATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAGTATATGGAAGAG  
GTGGGTTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGATTTAGTAATGTCA  
CTGTTTAACCAAGTTTGGATATTAGATGATCCTAACCAATTCACTATCCTGTGGCCTAAAG  
AGACAGGAATTGATATCCTTTATAAGGAAAAAAGTCTATTACAGGAGCCGAGCAGATTG  
CTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCTGTAGGTTGGAG

30841 GCAATTGCCCATTCAACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACA  
TCATTTCTTCTTTTTTCCCTCTCTTCTGTTGTCTCTAGGTGATGGCCATTGCCACTTTG  
GCTGCCTGTTATAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAGGGCAA  
GCAGTGACCCTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAG  
TATATGGAAGAGGTGGGTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGAT  
[G, T]  
TAGTAATGTCACTGTTTAACCAGGTTTGGATATTAGATGATCCTAACCAATTCATATCCT  
GTGGCCTAAAGAGACAGGAATTGATATCCTTTATAAGGAAAAAAGTCTATTACAGGAGC  
CGAGCAGATTGCTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCT  
GTAGGTTGGAGCCCTCAGTAGAATCATAGATTTTGAGCTGCAAGATGATGCAGGAGGCC  
AACCAAGCTTCTTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGCTGTGCTGATGCAG

31376 GAGGCCAACCAAGCTTCTTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTG  
ATGCAGTGCGTGATTGAGTGGATCTCTGGCTCCCGTCCATGTGTCTTGACACCCAGTCTG  
GTACTTTTATTATGCCACAGGCCCTCAATTGAAAAATCACAGTAGGGAATTTAGGCCAAGG  
AAAGCCATCAAGTTGCAATTATTTCTTAAATTTCTTTGGAAAAATTCATTTCAAATACC  
AAAACCATCCTATAAAAAAGAAAACCTTACCTTCTTAGGTCAAATCTCTAATATTTGACTAG  
[G, A]  
TTCAAAAAGTTTTATTTCTGGCCAGGCACAGTAGCTTACTCTGAAATCCCAGCACTTTGG  
GAGACCAAGGTGGGAGGATCACTTGAGGCCAGGAATCAAGACCAGCCGGGCGACATAG  
CAAGACCCCATTTCTACAAAAAATTTAAAAATTTGTCATGGTGGTGACGCCTGTGTGCTCC  
AGCTACTCAGGAGGCTGAGGCAGGTGGATCACATGAGCCTGAGAGGTGAGGCTACAGTA  
AGCTGTGTGATTTTCATCATTGCACTCTAGCCTGGGTGATAGAGTGAGACTTTGTCTCAA

FIGURE 3V

32032 TCTCTAGGCCCTAGAGCAGTGGTTTGTAAATGGAGGTGATTTGCTCCCCCTCCCCCAGAG  
GACATTGGACAATGTCTGGAGACATTTTTGATTGTCCTAACCGGCAGGAATCGGGTGCTA  
CTGGCATCTGGTGAGTAGAGGCCAGGATGATGCTGTGATCCTCAGGTGTGATCCTGTTG  
AGAATGAAACACTGTAGACTTTATGAAAACATACAAGACCCTCATCATTTTTCTTTGCC  
TGAGCTCCCTCCCCAGAGGTTACCTCTGTTTCATGGTTTTGTGCATCCGTCTAGTCCCCCT  
[A, G]  
TTACGCGTTTTACAGGAATATGGTTTGCAACAGTGTTCATCTAAATAGAATTATACAA  
ATAGCGATTTCTGATTTCTCTTGCATATTGCACATTCTTCTTATACTTCTCCCTACCTT  
TATCTGACACAGAAATGCTGTATGTCCAGAATTCTATCAGAGGCACCTATGGAAGTCTA  
AGGGAAGACCACATCGCTTTTAAAAACCTAAAATTTGTAGTCACTAGATGAAAATATT  
CAGCCAGTGACCCAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAA

32525 ATCGCTTTTAAAAACCTAAAATTTGTAGTCACTAGATGAAAATATTCAGCCAGTGACC  
CAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAACTTACTTTGATC  
TATGTGCCTGGGTAGTGACCAAGTAGGTGGGTAGGAGTAATCTCAGGGAAACTTGAGGC  
CCAGCCTCATGGCTAGGGTCATAATTTGAACCCAGGTCTGTCTGACATCAGAAATCCATG  
ATGTTAAACCCCAATTCTAAGGGGTTCAACTACCCTTTCTAAATGGAATCCTGCTATATTA  
[A, G]  
GCACTATTTATTCATTTTATATAAACTAGAAACATTTTATGTAGTAAGTAGTTGAGAGTG  
TTTTGGTTTTGTCAGTTTGATCACTAGTTTTAGAAACAGTTTTTAAACACTTTGTGGCCA  
ATTCATTACTATATTAATAATTCAGATTTATTTGGTTTTTCTTAACTATTGGGATTAA  
TCCTGGTTGTAATTCATAGTTTGAGGGCGAGGGTGGGCAGTCTACATTTGGCTGAGCCCT  
GTTTTTGTGAATAAATGTTATCAGAACACAGCCACACCCATTGCTTCTATGTCTTCTGT

34179 CTGCTGTATGTAGCACAGCATTGCACAAGAGCTTATTTTCAGTCTAGTAAACATTTATAGG  
AGCCTGTGTCAATTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCAAAACT  
TTGGGAGGCTGAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAAT  
ATGGCAAAACCCCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACACT  
TGTCATCCAGCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACTCGGGAGGTGGAG  
[G, T]  
TTGTAGTGAGCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTT  
TCTCAAACCTCCTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGAAAAGTCGG  
CTATGACCTGTCCCTTGACAAGCAGATGTAACCTCCTTGATTGAGGCTAGTAGGTTTTAAG  
ACCTGAATAATTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGG  
TTTGGTCTAGCAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGT

34249 ATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAACTTTGGGAGGCT  
GAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAATATGGCAAAAC  
CCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGCACACTTGTATCCCA  
GCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACTCGGGAGGTGGAGGTTGTAGTGA  
GCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACCT  
[T, C]  
CTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGAAAAGTCGGCTATGACCTG  
TCCTTGACAAGCAGATGTAACCTCCTTGATTGAGGCTAGTAGGTTTTAAGACCTGAATAA  
TTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTGGTCTAG  
CAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGT  
CTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTATGTTTATATGTTAGAAATGA

34451 GAGCATCGCTTGAACCTCGGAGGTGGAGGTTGTAGTGAGCTGAGATGGCACCCTGCACT  
CCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACCTCCTCAAGTATTTGGCTTCAACT  
TTATGCCGGGCATGTAGATGAAAAGTCGGCTATGACCTGTCTTGACAAGCAGATGTAAC  
TCCTTGATTGAGGCTAGTAGGTTTTAAGACCTGAATAATTGAGTTTGCAGAAACCTACT  
GTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGGTC  
[T, C]  
CTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGCTCTGAGTACCAGTGACTGCAGCT  
CTTCCAGTTGTGCTGTATGTTTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTT  
TGCCACTAATTGTATTACCGGGGACTGTACAACCAAGATTTCTCTAATTTATTCACCT  
TACTTATCTCCTGGAAGGGCATATTGAAGTGCTCTTGAGATTCTCTAAAAGGGTTTTTGT  
TGGTTGTGTATATCACTTGGGTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCC

34532 AGGCCCTTTCTCAAACCTCCTCAAGTATTTGGCTTCAACTTTATGCCGGGCATGTAGATGA

FIGURE 3W

AAAGTCGGCTATGACCTGTCTTGAACAAGCAGATGTAACCTCTTGATTGAGGCTAGTAGG  
TTTTTAAGACCTGAATAATTGAGTTTGCAGAAACCTACTGTGTGCCTTCAGGTAATGGA  
GAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTG  
TTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTCATG  
[T, C]  
TTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTTGGCCACTAATTGTATTACCGG  
GGACTGTCAACAACCAAGATTTCTCTTAATTTATTACCTTACTTATCTCCTGGAAGGGCA  
TATTGAAGTGCTCTTGGAGTTCTCTAAAAGGGTTTGTGTGGTTGTGTATATTCACTTGG  
GTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCCCAAAGGATGTAAGATGGCTT  
ATGGTTATAAGTACAACAGGCTAACAAAGTACAAGTAGATGAGAAAGTAAATGAAGAAA

36541 GGTAGGAGCCAGTTGAAGGGACGTGGGAGGCGCATTCCAGAGAGAAGGAGTGGTATGAGA  
CTGGAACAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTT  
TGTTTTTGTGTTGTTTTTGGAGACAGGGTCTTGTCTGTTCATCCAGGCTGGAGTGCAGTGG  
CATGATCTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCCACCCAGT  
CCCCAAGTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTGTACATT  
[T, C]  
TGTAAGAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAG  
TCTACATGCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCC  
CGGCAACTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGG  
TGCAGTAGGTCTGGACCATGGGTGGCCTTGCCTACACATTACAGAGCTCAGGCTTTTTT  
TCTCCAGGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGG

36607 CAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTTTGTGTTT  
TGTTTGTGTTTTTGGAGACAGGGTCTTGTCTGTTCATCCAGGCTGGAGTGCAGTGGCATGAT  
CTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCCACCCAGTCCCCAA  
GTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTGTACATTTTGTAG  
AAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTAC  
[A, G]  
TGCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCCGCAA  
CTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGT  
AGGTCTGGACCATGGGTGGCCTTGCCTACACATTACAGAGCTCAGGCTTTTTTCTCCA  
GGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAG  
TGTAAGACAGACAGGTAGATTTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATA

36681 GACAGGGTCTTGTCTGTTCATCCAGGCTGGAGTGCAGTGGCATGATCTCGGATCACTGCA  
ACCTCCACCTCCAGGCTCAAGTGATCTTCCCACCCAGTCCCCAAGTAGCTGGGGGACC  
ACAGGTGCATGCCACGATGCCCGGCTAATTTTGTACATTTTGTAGAAACAGGGTTTTAC  
TGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTACATGCCTCAGCCTCC  
TGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCCGCAACTGTTACTAGACT  
[A, G]  
TAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGTAGGTCTGGACCATG  
GGTGCCCTTGCCTACACATTACAGAGCTCAGGCTTTTTTCTCCAGGTGAGAGGGCTGG  
TGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAGTGTAGAGCAGACAG  
GTAGATTTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATAGCTCATCTGAGAGG  
CACTCAGGGCCTAATCTCAGGCAGTAATTTTAGGGATGTAGGGGAAGAGATGGATTCTGC

37493 TGACGTTTATTGGGCCTGGCACTGTGAGGTGCTGGGGATGTGAAGATCATTGTGGCTCAG  
CCGCTGCTCTCGAGGGCCTCTGGGTGCAGTATGCACACCTGTGCCTCCTGTTTGCTCAGG  
AAGACAGGCTTTGAGATGAGCTGGGGCTGACATCCCCACCTTATCATTGGGATGGCTTTG  
GGTAAGTTATGTTTCATGTTCTCTGAGCCTCCCTTTCTCATTGGTAAAATGGGTATAAAA  
TACCTGCCAGTGGAGGGTTGTTGTAAGTAGCCATGAAAATGTAAAGCACATAGCACTTA  
[C, T]  
CATTTTTTCTGTGTCTTTAACAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCT  
AGCAAAAACAAGGCAGATCATCTCCACCATCCGGACGCAGAATCTTCCCAACTGTCAGCTG  
ATTTCCCGAAGCACTACTCCCCATCTACCTGTCTGTTTGTCTGCTGTTTGGCTGCCTG  
AGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTTCACTGGAGAA  
CACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACTTTTTTCT

37966 CTGCCCTGAGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTTCA  
CTGGAGAACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTTACT  
TTTTTCTTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTACTACTTTAATCCCT

FIGURE 3X

AAAAGAACGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAA  
ACATGAAAGGAAAGGGTGCCTCATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTG  
[C, A]  
TGCTTGTGGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGT  
GACTGTCATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTTAAAGTATTTAA  
TTTGAAGCACCATTGAATGTTTCGTACTAGTAGAAAATGATGTGAATTTCTTTCTGTTC  
GGCTCCTATTTTTCTCATCATTTTTGTTTTCTTTAATTGGGTTGAATGGAGTAGATAGAAA  
TATTTATGGTTTAGGTAACAGTTAGATGTTTCTAAGAATGCAAACTGCCTTTTCCACAC

37973 GAGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTTCAGACTGGAGA  
ACACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTACTTTTTTTC  
TTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTACTACTTTAATCCCTAAAAGAA  
CGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAA  
AGGAAAGGGTGCCTCATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGCTTG  
[T, C]  
GGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTC  
ATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTTAAAGTATTTAATTTGAAG  
CACCATTGAATGTTTCGTACTAGTAGAAAATGATGTGAATTTTCTTTCTGTTTCGGCTCCT  
ATTTTTCTCATCATTTTTGTTTTCTTTAATTGGGTTGAATGGAGTAGATAGAAATATTTAT  
GGTTTAGGTAACAGTTAGATGTTTCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCT

38113 TCTCTTTATTTTTTCTCTACTACTTTAATCCCTAAAAGAACGCTGTGTGGCTGGGACCTT  
TAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCCTCATCCC  
AGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGCTTGTGGCTCATGGCAGAGCATT  
AGTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGATCCTACTTAGTAT  
GATCCTGGCTAGAATGATAATTTAAAGTATTTAATTTGAAGCACCATTGAATGTTTCGTA  
[C, A]  
TAGTAGAAAATGATGTGAATTTTCTTTCTGTTTCGGCTCCTATTTTTCTCATCATTTTTGTT  
TTCTTTAATTGGGTTGAATGGAGTAGATAGAAATATTTATGGTTTAGGTAACAGTTAGAT  
GTTTCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATTCTGGGTAT  
TCTCGTATTCTCATTTAAAGGAGTTTAGCTTTCAGAGAGAAACAGCAGGATTGCTTTTGA  
CCTTTTAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAAGAA

38298 CACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGAGATCCTACTTAGTATGATCC  
TGGCTAGAATGATAATTTAAAGTATTTAATTTGAAGCACCATTGAATGTTTCGTACTAGT  
AGAAAATGATGTGAATTTTCTTTCTGTTTCGGCTCCTATTTTTCTCATCATTTTTGTTTTCT  
TTAATTGGGTTGAATGGAGTAGATAGAAATATTTATGGTTTAGGTAACAGTTAGATGTTT  
CCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATTCTGGGTATTCTC  
[G, C]  
TATTCTCATTTAAAGGAGTTTAGCTTTCAGAGAGAAACAGCAGGATTGCTTTTGACCTTT  
TAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAAGAATTTAA  
TTGCTCTGCATTTGTCAAGTACAGTTTCGCTTGAAGCCTGCCTGACTGTGGAAAAGATGG  
AGCTCAAGAATGGAGTTGATGGCCAGCGTGGTGGCTCATGCCTGTAATCCCAGCACTTT  
GGGAGGCTGAGGCGGTTCGATCACGACATTAGGGGATCGAGACCATCCTGGCTAACACGG

FIGURE 3Y